



SEQUENCE LISTING

<110> Wright, David A.
Voytas, Daniel F.

<120> PLANT RETROELEMENTS AND METHODS RELATED THERETO

<130> P-1065A

<140> 09/586,106

<141> 2000-06-02

<150> 60/087,125

<151> 1998-05-29

<150> 09/322,478

<151> 1999-05-28

<160> 190

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 18

<212> DNA

<213> Glycine max

<400> 1

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18

<210> 2

<211> 18

<212> DNA

<213> Glycine max

<400> 2

tggcgccggtt gtcgggga

18

<210> 3

<211> 6

<212> DNA

<213> Glycine max

<400> 3

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6

<210> 4

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 4

Met Ala Ser Arg Lys Arg Lys

1

5

<210> 5

<211> 1263

<212> DNA

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 5

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atccttccag agaggaatgt agagcttgga ccagggatgt ttgatgagtt cctgcaggaa    180
ctccagaggc tcagatggga ccaggttctg acccgacttc cagagaagtg gattgatgtt    240
gctctggtga aggagtttta ctccaaccta tatgatccag aggaccacag tccgaagttt    300
tggagtgttc gaggacaggt tgtgagattt gatgctgaga cgattaatga tttcctcgac    360
accccggtca tcttggcaga gggagaggat tatccagcct actctcagta cctcagcact    420
cctccagacc atgatgccat cctttccgct ctgtgtactc cagggggacg atttgttctg    480
aatgttgata gtgccccctg gaagctgctg cggaaggatc tgatgacgct cgcgcagaca    540
tggagtgtgc tctcttattt taaccttgca ctgacttttc acacttctga tattaatgtt    600
gacagggccc gactcaatta tggttgggtg atgaagatgg acctggacgt gggcagcctc    660
atttctcttc agatcagtca gatcgcccag tccatcactt ccaggcttgg gttcccagcg    720
ttgatcacia cactgtgtga gattcagggg gttgtctctg ataccctgat ttttgagtca    780
ctcagtcctg tgatcaacct tgcctacatt aagaagaact gctggaaccc tgccgatcca    840
tctatcacat ttcaggggac ccgccgcacg cgcaccagag cttcggcgct gcctctgag    900
gctcctcttc catcccagca tccttctcag cctttttccc agagaccacg gcctccactt    960
ctatccacct cagcacctcc atacatgcat ggacagatgc tcaggtcctt gtaccagggg    1020
cagcagatca tcattcagaa cctgtatcga ttgtccctac atttgcagat ggatctgcca    1080
ctcatgactc cggaggccta tcgtcagcag gtcgccaagc taggagacca gccctccact    1140
gacagggggg aagagccttc tggagccgct gctactgagg atcctgccgt tgatgaagac    1200
ctcatagctg acttggctgg cgctgattgg agcccatggg cagacttggg cagaggcagc    1260
tga                                           1263

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<210> 6

<211> 421

<212> PRT

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 6

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Met Ala Ser Arg Lys Arg Lys Ala Val Pro Thr Pro Gly Glu Ala Ser
 1           5           10          15
Asn Trp Asp Ser Ser Arg Phe Thr Phe Glu Ile Ala Trp His Arg Tyr
          20          25          30
Gln Asp Ser Ile Gln Leu Arg Asn Ile Leu Pro Glu Arg Asn Val Glu
          35          40          45
Leu Gly Pro Gly Met Phe Asp Glu Phe Leu Gln Glu Leu Gln Arg Leu
          50          55          60
Arg Trp Asp Gln Val Leu Thr Arg Leu Pro Glu Lys Trp Ile Asp Val
65          70          75          80
Ala Leu Val Lys Glu Phe Tyr Ser Asn Leu Tyr Asp Pro Glu Asp His
          85          90          95
Ser Pro Lys Phe Trp Ser Val Arg Gly Gln Val Val Arg Phe Asp Ala
          100          105          110

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Glu Thr Ile Asn Asp Phe Leu Asp Thr Pro Val Ile Leu Ala Glu Gly
 115 120 125
 Glu Asp Tyr Pro Ala Tyr Ser Gln Tyr Leu Ser Thr Pro Pro Asp His
 130 135 140
 Asp Ala Ile Leu Ser Ala Leu Cys Thr Pro Gly Gly Arg Phe Val Leu
 145 150 155 160
 Asn Val Asp Ser Ala Pro Trp Lys Leu Leu Arg Lys Asp Leu Met Thr
 165 170 175
 Leu Ala Gln Thr Trp Ser Val Leu Ser Tyr Phe Asn Leu Ala Leu Thr
 180 185 190
 Phe His Thr Ser Asp Ile Asn Val Asp Arg Ala Arg Leu Asn Tyr Gly
 195 200 205
 Leu Val Met Lys Met Asp Leu Asp Val Gly Ser Leu Ile Ser Leu Gln
 210 215 220
 Ile Ser Gln Ile Ala Gln Ser Ile Thr Ser Arg Leu Gly Phe Pro Ala
 225 230 235 240
 Leu Ile Thr Thr Leu Cys Glu Ile Gln Gly Val Val Ser Asp Thr Leu
 245 250 255
 Ile Phe Glu Ser Leu Ser Pro Val Ile Asn Leu Ala Tyr Ile Lys Lys
 260 265 270
 Asn Cys Trp Asn Pro Ala Asp Pro Ser Ile Thr Phe Gln Gly Thr Arg
 275 280 285
 Arg Thr Arg Thr Arg Ala Ser Ala Ser Glu Ala Pro Leu Pro
 290 295 300
 Ser Gln His Pro Ser Gln Pro Phe Ser Gln Arg Pro Arg Pro Pro Leu
 305 310 315 320
 Leu Ser Thr Ser Ala Pro Pro Tyr Met His Gly Gln Met Leu Arg Ser
 325 330 335
 Leu Tyr Gln Gly Gln Gln Ile Ile Ile Gln Asn Leu Tyr Arg Leu Ser
 340 345 350
 Leu His Leu Gln Met Asp Leu Pro Leu Met Thr Pro Glu Ala Tyr Arg
 355 360 365
 Gln Gln Val Ala Lys Leu Gly Asp Gln Pro Ser Thr Asp Arg Gly Glu
 370 375 380
 Glu Pro Ser Gly Ala Ala Ala Thr Glu Asp Pro Ala Val Asp Glu Asp
 385 390 395 400
 Leu Ile Ala Asp Leu Ala Gly Ala Asp Trp Ser Pro Trp Ala Asp Leu
 405 410 415
 Gly Arg Gly Ser Glx
 420

<210> 7

<211> 1596

<212> DNA

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 7

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acctcacctc	ctccttctcc	aaattatgct	cagatggacg	gggaaccggc	acaaagagtc	180
acactagagg	acttctctaa	taccaccact	cctcagttct	ttacaagtat	cacaaggccg	240
gaagtccaag	cagatctcct	tactcaaggg	aacctcttcc	atggtcttcc	aatgaagat	300
ccatatgcgc	atctagcctc	atacatagag	atatgcagca	ccgttaaaat	cgccggagtt	360
ccaaaagatg	cgatactcct	taacctcttt	tccttttccc	tagcaggaga	ggcaaaaaga	420

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tggttgcaact ccttttaaagg caatagctta agaacatggg aagaagtagt ggaaaaattc 480
ttaaagaagt atttcccaga gtcaaagacc gtcgaacgaa agatggagat ttcttatttc 540
catcaatttc tggatgaatc ccttagcgaa gcaactagacc atttccacgg attgctaaga 600
aaaacaccaa cacacagata cagcgagcca gtacaactaa acatattcat cgatgacttg 660
caactcttaa tcgaaacagc tactagaggg aagatcaagc tgaagactcc cgaagaagcg 720
atggagctcg tcgagaacat ggcggctagc gatcaagcaa tccttcatga tcacacttat 780
gttcccacaa aaagaagcct cttggagctt agcacgcagg acgcaacttt ggtacaaaac 840
aagctgttga cgaggcagat agaagccctc atcgaaaccc tcagcaagct gcctcaacaa 900
ttacaagcga taagtcttct ccactcttct gttttgcagg tagaagaatg ccccatatgc 960
agagggacac atgagcctgg acaatgtgca agccaacaag acccctctcg tgaagtaa 1020
tatataggca tactaaatcg ttacggattt cagggctaca accagggaaa tccatctgga 1080
ttcaatcaag gggcaacaag atttaatcac gagccaccgg ggtttaatca aggaagaaac 1140
ttcatgcaag gctcaagttg gacgaataaa ggaaatcaat ataaggagca aaggaaccaa 1200
ccaccatacc agccaccata ccagcaccct agccaagggtc cgaatcagca agaaaagccc 1260
acaaaatag aggaactgct gctgcaattc atcaaggaga caagatcaca tcaaaagagc 1320
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gaacggccca ctagaacttt cgggtgctaac atggagagaa gaacccaag gaaggataaa 1440
gcagtactga ctagagggca gagaagagcg caggaggagg gtaagggtga aggagaagac 1500
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aagcgtacca agagccagag agcaagggaa gccaa 1596

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<210> 8

<211> 532

<212> PRT

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 8

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Met Arg Gly Arg Thr Ala Ser Gly Asp Val Val Pro Ile Asn Leu Glu
 1           5           10          15
Ile Glu Ala Thr Cys Arg Arg Asn Asn Ala Ala Arg Arg Arg Arg Glu
          20          25          30
Gln Asp Ile Glu Gly Ser Ser Tyr Thr Ser Pro Pro Pro Ser Pro Asn
          35          40          45
Tyr Ala Gln Met Asp Gly Glu Pro Ala Gln Arg Val Thr Leu Glu Asp
          50          55          60
Phe Ser Asn Thr Thr Thr Pro Gln Phe Phe Thr Ser Ile Thr Arg Pro
65          70          75          80
Glu Val Gln Ala Asp Leu Leu Thr Gln Gly Asn Leu Phe His Gly Leu
          85          90          95
Pro Asn Glu Asp Pro Tyr Ala His Leu Ala Ser Tyr Ile Glu Ile Cys
          100         105         110
Ser Thr Val Lys Ile Ala Gly Val Pro Lys Asp Ala Ile Leu Leu Asn
          115         120         125
Leu Phe Ser Phe Ser Leu Ala Gly Glu Ala Lys Arg Trp Leu His Ser
          130         135         140
Phe Lys Gly Asn Ser Leu Arg Thr Trp Glu Glu Val Val Glu Lys Phe
145         150         155         160
Leu Lys Lys Tyr Phe Pro Glu Ser Lys Thr Val Glu Arg Lys Met Glu
          165         170         175
Ile Ser Tyr Phe His Gln Phe Leu Asp Glu Ser Leu Ser Glu Ala Leu
          180         185         190
Asp His Phe His Gly Leu Leu Arg Lys Thr Pro Thr His Arg Tyr Ser
          195         200         205
Glu Pro Val Gln Leu Asn Ile Phe Ile Asp Asp Leu Gln Leu Leu Ile

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210		215		220
Glu Thr Ala Thr Arg Gly Lys Ile Lys Leu Lys Thr Pro Glu Glu Ala				
225		230		235
Met Glu Leu Val Glu Asn Met Ala Ala Ser Asp Gln Ala Ile Leu His				240
		245		250
Asp His Thr Tyr Val Pro Thr Lys Arg Ser Leu Leu Glu Leu Ser Thr				255
		260		265
Gln Asp Ala Thr Leu Val Gln Asn Lys Leu Leu Thr Arg Gln Ile Glu				270
		275		280
Ala Leu Ile Glu Thr Leu Ser Lys Leu Pro Gln Gln Leu Gln Ala Ile				285
		290		295
Ser Ser Ser His Ser Ser Val Leu Gln Val Glu Glu Cys Pro Thr Cys				300
305		310		315
Arg Gly Thr His Glu Pro Gly Gln Cys Ala Ser Gln Gln Asp Pro Ser				320
		325		330
Arg Glu Val Asn Tyr Ile Gly Ile Leu Asn Arg Tyr Gly Phe Gln Gly				335
		340		345
Tyr Asn Gln Gly Asn Pro Ser Gly Phe Asn Gln Gly Ala Thr Arg Phe				350
		355		360
Asn His Glu Pro Pro Gly Phe Asn Gln Gly Arg Asn Phe Met Gln Gly				365
		370		375
Ser Ser Trp Thr Asn Lys Gly Asn Gln Tyr Lys Glu Gln Arg Asn Gln				380
385		390		395
Pro Pro Tyr Gln Pro Pro Tyr Gln His Pro Ser Gln Gly Pro Asn Gln				400
		405		410
Gln Glu Lys Pro Thr Lys Ile Glu Glu Leu Leu Leu Gln Phe Ile Lys				415
		420		425
Glu Thr Arg Ser His Gln Lys Ser Thr Asp Ala Ala Ile Arg Asn Leu				430
		435		440
Glu Val Gln Met Gly Gln Leu Ala His Asp Lys Ala Glu Arg Pro Thr				445
		450		455
Arg Thr Phe Gly Ala Asn Met Glu Arg Arg Thr Pro Arg Lys Asp Lys				460
465		470		475
Ala Val Leu Thr Arg Gly Gln Arg Arg Ala Gln Glu Glu Gly Lys Val				480
		485		490
Glu Gly Glu Asp Trp Pro Glu Glu Gly Arg Thr Glu Lys Thr Glu Glu				495
		500		505
Glu Glu Lys Val Ala Glu Glu Pro Lys Arg Thr Lys Ser Gln Arg Ala				510
		515		520
Arg Glu Ala Lys				525
530				

<210> 9

<211> 603

<212> DNA

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 9

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tcatacggga atgtctacat cttggttagct gtggattacg tctccaaatg ggtggaagcc	180
atagccacgc caaaggacga tgccagggtg gtgatcaaat ttctgaagaa gaacattttt	240
tcccgttttg gagtcccacg agccttgatt agtgataggg gaacgcactt ctgcaacaat	300
cagttgaaga aagtcctgga gcactataat gtccgacata aggtggccac accttatcac	360

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cctcagacaa atggccaagc agaaatttct aacagggagc tcaagcgaat cctggaaaag 420
acagttgcat caacaagaaa ggattggtcc ttgaagctcg atgatgctct ctgggcctat 480
aggacagcgt tcaagactcc catcggctta tcaccatttc agctagtgtg tgggaaggca 540
gttcatttac cagtggagct ggagtacaaa gcatattggg ctctcaagtt gctcaacttt 600
gac 603

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<210> 10
 <211> 201
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> plant retroelement sequence

<400> 10
 Cys Asp Lys Cys Gln Arg Thr Gly Gly Ile Ser Arg Arg Asn Glu Met
 1 5 10 15
 Pro Leu Gln Asn Ile Met Glu Val Glu Ile Phe Asp Cys Trp Gly Ile
 20 25 30
 Asp Phe Met Gly Pro Phe Pro Ser Ser Tyr Gly Asn Val Tyr Ile Leu
 35 40 45
 Val Ala Val Asp Tyr Val Ser Lys Trp Val Glu Ala Ile Ala Thr Pro
 50 55 60
 Lys Asp Asp Ala Arg Val Val Ile Lys Phe Leu Lys Lys Asn Ile Phe
 65 70 75 80
 Ser Arg Phe Gly Val Pro Arg Ala Leu Ile Ser Asp Arg Gly Thr His
 85 90 95
 Phe Cys Asn Asn Gln Leu Lys Lys Val Leu Glu His Tyr Asn Val Arg
 100 105 110
 His Lys Val Ala Thr Pro Tyr His Pro Gln Thr Asn Gly Gln Ala Glu
 115 120 125
 Ile Ser Asn Arg Glu Leu Lys Arg Ile Leu Glu Lys Thr Val Ala Ser
 130 135 140
 Thr Arg Lys Asp Trp Ser Leu Lys Leu Asp Asp Ala Leu Trp Ala Tyr
 145 150 155 160
 Arg Thr Ala Phe Lys Thr Pro Ile Gly Leu Ser Pro Phe Gln Leu Val
 165 170 175
 Tyr Gly Lys Ala Cys His Leu Pro Val Glu Leu Glu Tyr Lys Ala Tyr
 180 185 190
 Trp Ala Leu Lys Leu Leu Asn Phe Asp
 195 200

<210> 11
 <211> 600
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> plant retroelement sequence

<400> 11
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 gttcccaaga aagggtggaat gacagtggta cgagatgaga ggaatgactt gataccaaca 120
 cgaactgtca ctggttggcg aatgtgtatc gactatcgca agctgaatga agccacacgg 180
 aaggaccatt tccccttacc tttcatggat cagatgctgg agagacttgc agggcaggca 240
 tactactgtt tcttggatgg atactcggga tacaaccaga tcgcggtaga ccccagagat 300
 caggagaaga cggcctttac atgccccttt ggcgtctttg cttacagaag gatgccattc 360

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gggttatgta atgcaccagc cacatttcag aggtgcatgc tggccatttt ttcagacatg      420
gtggagaaaa gcatcgaggt atttatggac gacttctcgg tttttggacc ctcatttgac      480
agctgtttga ggaacctaga gagggacttt cagaggtgcg aagagactaa cttggtactg      540
aattgggaaa agtgtcattt catggttcga gagggcatag tcctaggcca caagatctca      600

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<210> 12

<211> 200

<212> PRT

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 12

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Leu Glu Ala Gly Leu Ile Tyr Pro Ile Ser Asp Ser Ala Trp Val Ser
 1           5           10          15
Pro Val Gln Val Val Pro Lys Lys Gly Gly Met Thr Val Val Arg Asp
          20          25          30
Glu Arg Asn Asp Leu Ile Pro Thr Arg Thr Val Thr Gly Trp Arg Met
          35          40          45
Cys Ile Asp Tyr Arg Lys Leu Asn Glu Ala Thr Arg Lys Asp His Phe
 50          55          60
Pro Leu Pro Phe Met Asp Gln Met Leu Glu Arg Leu Ala Gly Gln Ala
65          70          75          80
Tyr Tyr Cys Phe Leu Asp Gly Tyr Ser Gly Tyr Asn Gln Ile Ala Val
          85          90          95
Asp Pro Arg Asp Gln Glu Lys Thr Ala Phe Thr Cys Pro Phe Gly Val
          100         105         110
Phe Ala Tyr Arg Arg Met Pro Phe Gly Leu Cys Asn Ala Pro Ala Thr
          115         120         125
Phe Gln Arg Cys Met Leu Ala Ile Phe Ser Asp Met Val Glu Lys Ser
          130         135         140
Ile Glu Val Phe Met Asp Asp Phe Ser Val Phe Gly Pro Ser Phe Asp
145         150         155         160
Ser Cys Leu Arg Asn Leu Glu Arg Val Leu Gln Arg Cys Glu Glu Thr
          165         170         175
Asn Leu Val Leu Asn Trp Glu Lys Cys His Phe Met Val Arg Glu Gly
          180         185         190
Ile Val Leu Gly His Lys Ile Ser
          195         200

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<210> 13

<211> 858

<212> DNA

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 13

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ccattcgggg aagccttaca gcagatgccc ctctactcca aatttatgaa agacatcctc      180
accaagaagg ggaagtatat tgacaacgag aatattgttg taggaggcaa ttgcagtgcg      240
ataatacaaaa ggattctacc caagaagttt aaagaccccg gaagtgttac catcccgtgc      300
accattggga aggaagccgt aaacaaggcc ctcattgatc taggagcaag tatcaatctg      360
atgcccttgt caatgtgcaa aagaattggg aatttgaaga tagatcccac caagatgacg      420

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cttcaactgg cagaccgctc aatcacaagg ccatatgggg tggtagaaga tgccttggtc 480
aaggtagccc acttcacttt tccggtggac tttgttatca tggatatcga agaagacact 540
gagattcccc ttatcttagg cagacccttc atgctgactg ccaactgtgt ggtggatatg 600
gggaaaggga acttagagtt gactattgat aatcagaaga tcacctttga cttatcaag 660
gcaatgaagt acccacagga gggttggaag tgcttcagaa tagaggagat tgatgaggaa 720
gatgtcagtt ttctcgagac accaaagact tcgctagaaa aagcaatggt aaatcattta 780
gactgtctaa ccagtgaaga ggaagaagat ctgaaggctt gcttggaaaa cttggatcaa 840
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<210> 14

<211> 286

<212> PRT

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 14

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Pro Thr Lys Lys Asn Lys Glu Arg Tyr Phe Ala Arg Phe Leu Glu Ile
20      25      30
Phe Lys Gly Leu Glu Ile Thr Met Pro Phe Gly Glu Ala Leu Gln Gln
35      40      45
Met Pro Leu Tyr Ser Lys Phe Met Lys Asp Ile Leu Thr Lys Lys Gly
50      55      60
Lys Tyr Ile Asp Asn Glu Asn Ile Val Val Gly Gly Asn Cys Ser Ala
65      70      75      80
Ile Ile Gln Arg Ile Leu Pro Lys Lys Phe Lys Asp Pro Gly Ser Val
85      90      95
Thr Ile Pro Cys Thr Ile Gly Lys Glu Ala Val Asn Lys Ala Leu Ile
100     105     110
Asp Leu Gly Ala Ser Ile Asn Leu Met Pro Leu Ser Met Cys Lys Arg
115     120     125
Ile Gly Asn Leu Lys Ile Asp Pro Thr Lys Met Thr Leu Gln Leu Ala
130     135     140
Asp Arg Ser Ile Thr Arg Pro Tyr Gly Val Val Glu Asp Val Leu Val
145     150     155     160
Lys Val Arg His Phe Thr Phe Pro Val Asp Phe Val Ile Met Asp Ile
165     170     175
Glu Glu Asp Thr Glu Ile Pro Leu Ile Leu Gly Arg Pro Phe Met Leu
180     185     190
Thr Ala Asn Cys Val Val Asp Met Gly Lys Gly Asn Leu Glu Leu Thr
195     200     205
Ile Asp Asn Gln Lys Ile Thr Phe Asp Leu Ile Lys Ala Met Lys Tyr
210     215     220
Pro Gln Glu Gly Trp Lys Cys Phe Arg Ile Glu Glu Ile Asp Glu Glu
225     230     235     240
Asp Val Ser Phe Leu Glu Thr Pro Lys Thr Ser Leu Glu Lys Ala Met
245     250     255
Val Asn His Leu Asp Cys Leu Thr Ser Glu Glu Glu Glu Asp Leu Lys
260     265     270
Ala Cys Leu Glu Asn Leu Asp Gln Glu Asp Ser Ile Pro Glu
275     280     285

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<210> 15

<211> 192

<212> DNA
 <213> Artificial Sequence

<220>
 <223> plant retroelement sequence

<400> 15
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 gacaagggtat ttcacgccat ctattatgct agcaagggtcc tgaatgaagc acagttgaat 120
 tatgcaacca cagaaaagga gatgctagcc attgtctttg ccttggagaa gttcagggtca 180
 tacttgatag gg 192

<210> 16
 <211> 64
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> plant retroelement sequence

<400> 16
 Phe Glu Leu Met Cys Asp Ala Ser Asp Tyr Ala Val Gly Ala Val Leu
 1 5 10 15
 Gly Gln Arg Lys Asp Lys Val Phe His Ala Ile Tyr Tyr Ala Ser Lys
 20 25 30
 Val Leu Asn Glu Ala Gln Leu Asn Tyr Ala Thr Thr Glu Lys Glu Met
 35 40 45
 Leu Ala Ile Val Phe Ala Leu Glu Lys Phe Arg Ser Tyr Leu Ile Gly
 50 55 60

<210> 17
 <211> 12286
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> plant retroelement sequence

<400> 17
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 ttaattattt agcagttatt tgtgattaaa agttagaaaa gcaattaagt tgaatttttg 120
 gccatagata tgaaaactga aggtacaaca agcaaaaaggc agcagaaaagt gaagaaaaag 180
 aataaaatct gaagcagacc cagcccaaca gcgcgccctta gcgcgcgtca cgcgctaagc 240
 ttgcaaggca gcacaggcac taagcgaggc gttaagcacg aagatgcagg attcgttacg 300
 tgcgctaagc gcgaggcaca cgctaagcgc gcgatccaac agaagcacac gctaagcctg 360
 cagcatgcgc taagcgcgcc tacgaaggcc caaagcccat ttctacacct ataaatagag 420
 atccaagcca agggagaatg tacaccttgc ctacagagcac ttctctcagc attccaagct 480
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 agttgtaaag cccctcaatg gccatgagtg gttaatcccc tagctacggc ctggtaggcc 600
 taaaaagcca atgatgtatg gtgtacttca agagttatca atgcaaagag gattcattcc 660
 aggttttatg ttctaattct ttccttttta tcttgcattt atgtcttaaa tttctgttg 720
 gttttattcg ctcgggagag ggtatttctt aataagggtt taagaagtaa tgcatgcatc 780
 agtttttaggg gttatacgct tggtaaaggg taacacctaa tagaacaat taagaaaagg 840
 atcgtcgggc tagcattgct aggcatagaa tgatggccca atgcccatgc atttagcaac 900
 atctagaatt taaccttaat gcattttaat tattgaatct tcacaaaggc atttgggaga 960
 taggtagtta aaataggctt gtcatcgtga ggcatcaagg gcaagtaaaa ttaatagatg 1020
 tgggtagaac taattcaact gcattggtaa tgaacatcat aaattcattc atcgtaggcc 1080

aattaggttt	gtccggtctt	ggcattttca	tcaattgtct	tcctaaatta	tttgatctaa	1140
tagcaacaat	ttattcttat	gcctattcct	gtttttacta	tttactttta	cttacaaatt	1200
gaagagtatt	caataaagt	caataaaaac	cctatggaaa	cgatactcgg	acttccgaga	1260
attactactt	agaacgattt	ggtacacttg	tcaaacacct	caacaagttt	ttggcgccgt	1320
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<211> 1857

<212> DNA

<213> Arabidopsis thaliana

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<210> 26

<211> 564

<212> DNA

<213> *Arabidopsis thaliana*

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<210> 27

<211> 180

<212> DNA

<213> *Arabidopsis thaliana*

<400> 27

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<210> 28

<211> 192

<212> DNA

<213> *Arabidopsis thaliana*

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<210> 29

<211> 597

<212> DNA

<213> *Pisum sativum*

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 <211> 192
 <212> DNA
 <213> Pisum sativum

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<210> 32
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1362

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cgaacagtca	ctggctggcg	aatgtgtatt	gactatcaca	agctgaatga	agctacacgg	180
aaggaccatt	ttcccttacc	tttcatggat	cagatgctgg	agagacttgc	agggcaggca	240
tactactgtt	tcttggatgg	atactcggga	tacaaccaga	tcgcggtaga	ccccatagat	300
caggagaaga	cggtctttac	atgccccttt	ggcgtctttg	cttacagaag	gatgtcattc	360
gggttatgta	atgtaccagc	cacatttcag	aggtgcatgc	tgaccatttt	ttcagacatg	420
gtggagaaaa	gcatacgaggt	atztatggac	gacttctcgg	tttttggacc	ctcatttgac	480
agctgtttga	ggaacctaga	aatggacttt	cagaggtgcg	tagagactaa	cttgggtactg	540
aattgggaaa	agtgtcattt	tatggttcga	gagggcatag	tcctaggcca	caagatc	597

<210> 35

<211> 603

<212> DNA

<213> Glycine max

<400> 35

tgtgataaat	gtcagagaa	aagggggata	tctcgaagaa	atgagatgcc	tttgcagaat	60
atcatggagg	tagagatctt	tgatagttgg	ggcatagact	tcattggggc	tcttccttca	120
tcatacagga	atgtctacat	cttggtagct	gtggattacg	tctccaaatg	ggtggaagcc	180
atagccacgc	tgaaggacga	tgccagggtg	gtgatcaaat	ttctgaagaa	gaacattttt	240
tcccatttctg	gagtcccacg	agccttgatt	agtgatgggg	gaacgcactt	ctgcaacaat	300
cagttgaaga	aagtccctgga	gcactataat	gtccgacaca	aggtggccac	accttatcac	360
actcagacga	atggccaagc	agaaatttct	aacaggggagc	tcaagcgaat	cctggaaaag	420
acagttgcat	catcaagaaa	ggattggggc	ttgaagctcg	atgatactct	ctgggcctat	480
aggacagcgt	tcaagactcc	catcggctta	tcaccatttc	agctagtata	tgggaaggca	540
tgtcattttac	cagtagagct	ggagcacaag	gcataattggg	ctctcaagtt	gctcaacttt	600
gac						603

<210> 36

<211> 150

<212> DNA

<213> Glycine max

<400> 36

cctaaaatac	tacaacgaca	tgattgggtg	tttaggataa	ttgactgaaa	aacctattat	60
caatttggcg	ccgttgccaa	ttgggtgttt	gtttgttaca	tttgagattt	cagacttgct	120
tagatcaagt	tctttttcaa	ttttcttttt				150

<210> 37
 <211> 11
 <212> DNA
 <213> Glycine max

<400> 37
 tggcgccggtt g 11

<210> 38
 <211> 15
 <212> DNA
 <213> Glycine max

<400> 38
 tggcgccggtt gccgg 15

<210> 39
 <211> 27
 <212> DNA
 <213> Glycine max

<400> 39
 tttttggcgc cggtgtcggg gattttg 27

<210> 40
 <211> 9
 <212> DNA
 <213> Glycine max

<400> 40
 tttggggga 9

<210> 41
 <211> 16
 <212> DNA
 <213> Glycine max

<400> 41
 tttaatttgg gggatt 16

<210> 42
 <211> 775
 <212> DNA
 <213> Nicotiana tabacum

<400> 42
 gtgcgtaaaag aggttttttaa actggagatt atcaagtgat tggatgccgg gggtatctac 60
 cccattttacg atagttcatg aacttctccg gtgcaatgtg tcccaaagaa ggtggcatga 120
 cgggtggtcac caatgagaag aatgagttga ttcctacaag aatgggtgacc gggtggagag 180
 tgtgcatgga ctatcgcaag ctcaacaaac tcacaaggaa ggatcatttc ccatttccat 240
 tccttgacca aatgcttgat aggttggcat gtcgtgcttt ctattgcttt ctagatgtat 300
 agtcgggcta tagccaaatc tttattgctc cgtaggatca cgagaaaata cctttacatg 360
 tccctatggg acttttgcct acaagcggat gccatttggg ttgtgtaatg cactagcgaa 420
 cttttatagg tgtatgatgg ctatcttcac ggacatgggt aaggactacc ttaaagtttt 480
 catggatgac ttctcgatgg ttggggattc ctttgatgat tgcttggaat atttggataa 540
 agtattggca agatatgaag aaacgaattt ggtactaaat tgggagaagt gtcatttcat 600

```

gatcgaggaa ggcattgttc ttggccacaa gatctcaaat aatggcattg aagtcgacaa      660
ggcaaaagatt aaggtgattt ctaaacttac acctccaact ttggtgaaag gcgtgcggag      720
tttcttaggc cacgcggggt tttaccaatt cttcataaaa gatttcacaa aggtt          775

```

<210> 43

<211> 259

<212> PRT

<213> Nicotiana tabacum

<400> 43

```

Val Arg Lys Glu Val Phe Lys Leu Glu Ile Ile Lys Glx Leu Asp Ala
 1           5           10           15
Gly Val Ile Tyr Pro Ile Tyr Asp Ser Ser Glx Thr Ser Pro Val Gln
          20           25           30
Cys Val Pro Lys Lys Gly Gly Met Thr Val Val Thr Asn Glu Lys Asn
          35           40           45
Glu Leu Ile Pro Thr Arg Met Val Thr Gly Trp Arg Val Cys Met Asp
          50           55           60
Tyr Arg Lys Leu Asn Lys Leu Thr Arg Lys Asp His Phe Pro Phe Pro
65           70           75           80
Phe Leu Asp Gln Met Leu Asp Arg Leu Ala Cys Arg Ala Phe Tyr Cys
          85           90           95
Phe Leu Asp Val Glx Ser Gly Tyr Ser Gln Ile Phe Ile Ala Pro Glx
          100          105          110
Asp His Glu Lys Thr Thr Phe Thr Cys Pro Tyr Gly Thr Phe Ala Tyr
          115          120          125
Lys Arg Met Pro Phe Gly Leu Cys Asn Ala Leu Ala Asn Phe Tyr Arg
          130          135          140
Cys Met Met Ala Ile Phe Thr Asp Met Val Lys Asp Tyr Leu Lys Val
145          150          155          160
Phe Met Asp Asp Phe Ser Met Val Gly Asp Ser Phe Asp Asp Cys Leu
          165          170          175
Glu Asn Leu Asp Lys Val Leu Ala Arg Tyr Glu Glu Thr Asn Leu Val
          180          185          190
Leu Asn Trp Glu Lys Cys His Phe Met Ile Glu Glu Gly Ile Val Leu
          195          200          205
Gly His Lys Ile Ser Asn Asn Gly Ile Glu Val Asp Lys Ala Lys Ile
          210          215          220
Lys Val Ile Ser Lys Leu Thr Pro Pro Thr Leu Val Lys Gly Val Arg
225          230          235          240
Ser Phe Leu Gly His Ala Gly Phe Tyr Gln Phe Phe Ile Lys Asp Phe
          245          250          255
Thr Lys Val

```

<210> 44

<211> 761

<212> DNA

<213> Nicotiana tabacum

<400> 44

```

gtgcgtaaaag aggtgggtcaa gctgttggat gtcgggggttg tgtaccccat ctctgatagc      60
tcttggactt cgccgggtgca atgtgtacca aagaagggttg gcatgactgt ggtgaaaaat      120
tccaaaaatg agttgattcc gacaagaacc atcaccgggtt ggagggtatg catggactac      180
cgcaagttga ataaagtgac ctgcaaggat cactttcctt tgccatttct ggatcagatg      240
ctagatcgac ttgctgggcg tgccttctat tgcttcttgg atgaatattc tgggtataac      300
caaatcttga ttgctccgga agatccggaa aagaccacat tcacttgtcc gtatggcaca      360

```

```

tttgttttct ctaggatgcc ttttaggttg tgtaatgcac cagctacatt tcagcgggtg 420
atgatggcca ttttctccta tatggtgaaa gacatttttg aggtgttcat ggacgatttt 480
agtgttggtg ggcactcatt tgatgaatgc ttgaagaatc ttgatagggt gttggcccat 540
tgtgaagaaa ccaatcttgt cctcaattgg gagaaatgcc actttatggt agaagaagga 600
atcaatctct ggcataaaat ttcaaaacat ggcattgagg tggataaaca aagatagatg 660
tgatttcaag gtcctctccc cctacatccg tcaagggagt ccgatgtttt cttgggcatg 720
cgggggttcta ttggagattc ataaaagact tctccaaggt t 761

```

<210> 45

<211> 254

<212> PRT

<213> Nicotiana tabacum

<400> 45

```

Val Arg Lys Glu Val Val Lys Leu Leu Asp Val Gly Val Val Tyr Pro
1      5      10      15
Ile Ser Asp Ser Ser Trp Thr Ser Pro Val Gln Cys Val Pro Lys Lys
20      25      30
Val Gly Met Thr Val Val Lys Asn Ser Lys Asn Glu Leu Ile Pro Thr
35      40      45
Arg Thr Ile Thr Gly Trp Arg Val Cys Met Asp Tyr Arg Lys Leu Asn
50      55      60
Lys Val Thr Cys Lys Asp His Phe Pro Leu Pro Phe Leu Asp Gln Met
65      70      75      80
Leu Asp Arg Leu Ala Gly Arg Ala Phe Tyr Cys Phe Leu Asp Glu Tyr
85      90      95
Ser Gly Tyr Asn Gln Ile Leu Ile Ala Pro Glu Asp Pro Glu Lys Thr
100     105     110
Thr Phe Thr Cys Pro Tyr Gly Thr Phe Val Phe Ser Arg Met Pro Phe
115     120     125
Arg Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile
130     135     140
Phe Ser Tyr Met Val Lys Asp Ile Phe Glu Val Phe Met Asp Asp Phe
145     150     155     160
Ser Val Val Gly His Ser Phe Asp Glu Cys Leu Lys Asn Leu Asp Arg
165     170     175
Val Leu Ala His Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
180     185     190
Cys His Phe Met Val Glu Glu Gly Ile Asn Leu Trp His Lys Ile Ser
195     200     205
Lys His Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Ser Arg
210     215     220
Leu Pro Pro Pro Thr Ser Val Lys Gly Val Arg Cys Phe Leu Gly His
225     230     235     240
Ala Gly Phe Tyr Trp Arg Phe Ile Lys Asp Phe Ser Lys Val
245     250

```

<210> 46

<211> 762

<212> DNA

<213> Nicotiana tabacum

<400> 46

```

gtgcgtaagg aggtgtttta gttgttggat gttgggggttg tgtaccccat ctctgatagc 60
tcttgcatth cgccgggtgca atgtgtaccg aagaaggggtg gcatgaccgt ggttgcaaat 120
tcgcaaaatg gggttgattcc taccaggatc gtcaccgggt ggaagggtatg catggattac 180
cgaaagttga ataaagtgac ccgcaaggat cactttccat tgctttttct tgatcagatg 240

```

```

ttagatcgac ttgctgggcg tgccttctac tgtttcttgg atgggtattc tggatacaac 300
caaatcttca ttactccgga agatcaggag aagacaacat tcacttgtec atatggcacc 360
tttgcttttt ctaggatgcc ttttgggttg tgtaatgcac cgactacatt ctagcgggat 420
atgatggcca ttttcactga tatgggtggaa gatattttgg aggtgttcat ggacgacttt 480
agtgttgtgg gtgattcatt tgatgaatgt ttgaataatc ttgatagagt gttggcccat 540
tgtaaagaaa ccaatcttgt tcttaattgg gagaaatgcc acttcatggg tgaggagggc 600
atagtcttgg ggcataaaat tttaaagcat ggtatagagg tggacaaagc aaaaattgat 660
gtgatttcaa ggctccctcc ccctacttct gtcaaggagg tgagaagttt tcttaggcat 720
gcgggggttct accggagatt catcaaagat ttcaccaaag tt 762

```

<210> 47

<211> 254

<212> PRT

<213> Nicotiana tabacum

<400> 47

```

Val Arg Lys Glu Val Phe Lys Leu Leu Asp Val Gly Val Val Tyr Pro
1          5          10          15
Ile Ser Asp Ser Ser Cys Ile Ser Pro Val Gln Cys Val Pro Lys Lys
20          25          30
Gly Gly Met Thr Val Val Ala Asn Ser Gln Asn Gly Leu Ile Pro Thr
35          40          45
Arg Ile Val Thr Gly Trp Lys Val Cys Met Asp Tyr Arg Lys Leu Asn
50          55          60
Lys Val Thr Arg Lys Asp His Phe Pro Leu Pro Phe Leu Asp Gln Met
65          70          75          80
Leu Asp Arg Leu Ala Gly Arg Ala Phe Tyr Cys Phe Leu Asp Gly Tyr
85          90          95
Ser Gly Tyr Asn Gln Ile Phe Ile Thr Pro Glu Asp Gln Glu Lys Thr
100          105          110
Thr Phe Thr Cys Pro Tyr Gly Thr Phe Ala Phe Ser Arg Met Pro Phe
115          120          125
Gly Leu Cys Asn Ala Pro Thr Thr Phe Glx Arg Tyr Met Met Ala Ile
130          135          140
Phe Thr Asp Met Val Glu Asp Ile Leu Glu Val Phe Met Asp Asp Phe
145          150          155          160
Ser Val Val Gly Asp Ser Phe Asp Glu Cys Leu Asn Asn Leu Asp Arg
165          170          175
Val Leu Ala His Cys Lys Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
180          185          190
Cys His Phe Met Val Glu Glu Gly Ile Val Leu Gly His Lys Ile Leu
195          200          205
Lys His Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Ser Arg
210          215          220
Leu Pro Pro Pro Thr Ser Val Lys Gly Val Arg Ser Phe Leu Arg His
225          230          235          240
Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
245          250

```

<210> 48

<211> 760

<212> DNA

<213> Nicotiana tabacum

<400> 48

```

gcggaaggag gtcgtcaagc tgttggatgt cggtgttgtg taccccatat ttgatagctc 60
ttggactttg ccggtgcaat atgtgccgaa gaagggtggt atgaccgtgg ttaccaatgt 120

```

```

aaaaaatgag ttgattccta ccaggactgt caccgggtgg aggggtgtgca tggattacca 180
caaattgaat aaagtgacct gcaaggatca ctttccatta ctttttcttg atcagatggt 240
agacagactt gctgggtgtg ccttctactg tttcttggat ggggtattctg ggtgcaacaa 300
aattttgatt gcacccaaaag atcaggagaa gaccaccttt acttgtagct atggtacctt 360
tgtcttttct aggatgtcat ttgggttgtg taatgcaccg actacattct agaggtgtat 420
gatggccata ttacctaca tgggtggagga cattttggag gtgtttatgg atgacttcag 480
tgttgttggg gactagtttg atgaatgttt gaaaaatcct gatagagtgt tggcccgtg 540
tgaagaagcc aaccttgtgc ttaattggga gaaatgccac ttcattggtg aggagggcat 600
agtccttagc cataaaattt caaagcatgg tatagaggtg gacaaagcaa aaattgaagt 660
gatttcaagg ctcttctccc ctacttctgt caaggaggtt agaagttttc ttgggcatgc 720
ggggttctac tggagattca tcaaagactt cacgaaggtt 760

```

<210> 49

<211> 253

<212> PRT

<213> Nicotiana tabacum

<400> 49

```

Arg Lys Glu Val Val Lys Leu Leu Asp Val Gly Val Val Tyr Pro Ile
1      5      10      15
Phe Asp Ser Ser Trp Thr Leu Pro Val Gln Tyr Val Pro Lys Lys Gly
20      25      30
Gly Met Thr Val Val Thr Asn Val Lys Asn Glu Leu Ile Pro Thr Arg
35      40      45
Thr Val Thr Gly Trp Arg Val Cys Met Asp Tyr His Lys Leu Asn Lys
50      55      60
Val Thr Arg Lys Asp His Phe Pro Leu Pro Phe Leu Asp Gln Met Leu
65      70      75      80
Asp Arg Leu Ala Gly Cys Ala Phe Tyr Cys Phe Leu Asp Gly Tyr Ser
85      90      95
Gly Cys Asn Lys Ile Leu Ile Ala Pro Lys Asp Gln Glu Lys Thr Thr
100     105     110
Phe Thr Cys Thr Tyr Gly Thr Phe Val Phe Ser Arg Met Ser Phe Gly
115     120     125
Leu Cys Asn Ala Pro Thr Thr Phe Glx Arg Cys Met Met Ala Ile Phe
130     135     140
Thr Tyr Met Val Glu Asp Ile Leu Glu Val Phe Met Asp Asp Phe Ser
145     150     155     160
Val Val Gly Asp Glx Phe Asp Glu Cys Leu Lys Asn Leu Asp Arg Val
165     170     175
Leu Ala Arg Cys Glu Glu Ala Asn Leu Val Leu Asn Trp Glu Lys Cys
180     185     190
His Phe Met Val Glu Glu Gly Ile Val Leu Ser His Lys Ile Ser Lys
195     200     205
His Gly Ile Glu Val Asp Lys Ala Lys Ile Glu Val Ile Ser Arg Leu
210     215     220
Leu Pro Pro Thr Ser Val Lys Gly Val Arg Ser Phe Leu Gly His Ala
225     230     235     240
Gly Phe Tyr Trp Arg Phe Ile Lys Asp Phe Thr Lys Val
245     250

```

<210> 50

<211> 762

<212> DNA

<213> Oryza sativa

<400> 50


```

gtgcgtaagg aggtgttttaa gttcctgtat gccaggatta tttatctcgt accatacagc      60
gagtgggtta gcccagttca ggtcgtgccca aagaaggag gaatgacggc cgttgcaa      120
gctcaaaatg aactaatccc gcaacgaacc gtaaccggat ggagaatgtg catcgattac      180
aggaaactta acaaggctac aaaaaaggat catttccgcg tacccttcat tgatgaaatg      240
ttggaacggc tggcaaataca ttccttcttc tgtttccttg atgggtattc aggatatcat      300
caaattccca tccatccgga ggaccagagt aagactacgt tcacatgtcc atatggcacc      360
tatgcgtatc gtaggatgcc ctttggactg tgcaacactc ctgcatcttt ccaaagggtg      420
atgatgtcta ttttctcgga catgatcgag gatatcatgg aagtcttcat ggatgacttc      480
tcggtctatg gaaagacttt gggtcattgt ctgcagaatc tagacaaagt cttacaacga      540
tgccaagaaa aggacctagt gcttaactgg gaaaagtgcc atttcatggg ctgtgaaggg      600
atagttcttg ggcacgcagt gtccgaacga ggagtcgaag ttgatcgtgc taaaattgat      660
gtgatagatc agcttctcc acccgatgaac atcaaaggaa tccgcagctt ctttggtcac      720
gctggctttt atagaagggt catcaaggac ttcacaaaag tt                                762

```

<210> 51

<211> 254

<212> PRT

<213> Oryza sativa

<400> 51

```

Val Arg Lys Glu Val Phe Lys Phe Leu Tyr Ala Arg Ile Ile Tyr Leu
1          5          10          15
Val Pro Tyr Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
20          25          30
Gly Gly Met Thr Ala Val Ala Asn Ala Gln Asn Glu Leu Ile Pro Gln
35          40          45
Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
50          55          60
Lys Ala Thr Lys Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met
65          70          75          80
Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr
85          90          95
Ser Gly Tyr His Gln Ile Pro Ile His Pro Glu Asp Gln Ser Lys Thr
100         105         110
Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr Arg Arg Met Pro Phe
115         120         125
Gly Leu Cys Asn Thr Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile
130         135         140
Phe Ser Asp Met Ile Glu Asp Ile Met Glu Val Phe Met Asp Asp Phe
145         150         155         160
Ser Val Tyr Gly Lys Thr Leu Gly His Cys Leu Gln Asn Leu Asp Lys
165         170         175
Val Leu Gln Arg Cys Gln Glu Lys Asp Leu Val Leu Asn Trp Glu Lys
180         185         190
Cys His Phe Met Val Cys Glu Gly Ile Val Leu Gly His Arg Val Ser
195         200         205
Glu Arg Gly Val Glu Val Asp Arg Ala Lys Ile Asp Val Ile Asp Gln
210         215         220
Leu Pro Pro Pro Val Asn Ile Lys Gly Ile Arg Ser Phe Phe Gly His
225         230         235         240
Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
245         250

```

<210> 52

<211> 761

<212> DNA

<213> Oryza sativa

<400> 52

```

gtgcgcaagg aggttttgaa attgctgcat gccaggatta tctatcccggt accatacagt      60
gagagggtta gccagtgcca ggttggtgcca aagaagggag gaatggcggg cgttgcaaat      120
gctcagaatg aactaattac gcaacaaacc gtaaccggat ggaggatgtg tatcgattac      180
aggaaactca acaaggctac aaaaaaggat catttcccg cacccttcat tgttgaaatg      240
ttggaacggc tggcaaatca ttccttcttt tgtttccttg atggatattt cggatatcat      300
caaattccca tccatccgga ggactagagt aagactacgt tcacatgtcc atatggcacc      360
tatgcgtatc ataggatgtc ctttggactg tgcaacgctc ctgcatcttt ccaagggtga      420
tgatgtctat tttctcggac atgatcgagg atatcatgga agtcttcatg gatgacttct      480
cggctctatg aaagactttc ggtcattgtc tgcaaaatct agacaaagtc ttacaacgat      540
gccaagaaaa ggacctgggtg cttaactggg aaaagtgaca tttcatggtc cgtgaaggga      600
tagttcttgg gcatcgagtg ttcgaacaag gaatcgaagt tgatcatgct aaaattgatg      660
tgatagatca gcttcctcct cccgtgaaca tcaaagggtat ccgcagcttc ttgggtcatg      720
tcggctttta tagaagggtc atcaaggact tcactaaagt t                                761

```

<210> 53

<211> 254

<212> PRT

<213> *Oryza sativa*

<400> 53

```

Val Arg Lys Glu Val Leu Lys Leu Leu His Ala Arg Ile Ile Tyr Pro
1          5          10          15
Val Pro Tyr Ser Glu Arg Val Ser Pro Val Gln Val Val Pro Lys Lys
20          25          30
Gly Gly Met Ala Val Val Ala Asn Ala Gln Asn Glu Leu Ile Thr Gln
35          40          45
Gln Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
50          55          60
Lys Ala Thr Lys Lys Asp His Phe Pro Leu Pro Phe Ile Val Glu Met
65          70          75          80
Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr
85          90          95
Phe Gly Tyr His Gln Ile Pro Ile His Pro Glu Asp Glx Ser Lys Thr
100          105          110
Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr His Arg Met Ser Phe
115          120          125
Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile
130          135          140
Phe Ser Asp Met Ile Glu Asp Ile Met Glu Val Phe Met Asp Asp Phe
145          150          155          160
Ser Val Tyr Gly Lys Thr Phe Gly His Cys Leu Gln Asn Leu Asp Lys
165          170          175
Val Leu Gln Arg Cys Gln Glu Lys Asp Leu Val Leu Asn Trp Glu Lys
180          185          190
Glx His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Arg Val Phe
195          200          205
Glu Gln Gly Ile Glu Val Asp His Ala Lys Ile Asp Val Ile Asp Gln
210          215          220
Leu Pro Pro Pro Val Asn Ile Lys Gly Ile Arg Ser Phe Leu Gly His
225          230          235          240
Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
245          250

```

<210> 54

<211> 762

<212> DNA

<213> Oryza sativa

<400> 54

```

gtgcggaaag aggtttttaaa gtcctgcat gccgggatta tttataaccgt tccatgcagt      60
gagtgggtca gcacagtcca ggttgggccg aagatgggat gaatgacggt cgttgcaaatt      120
gctcaaaata aacttatccc gcaaccaacc ataaccggat ggaggatgtg catagactac      180
aggaaactca acaaggctac aaaagaggat cattttccgc tacccttcat tgatgaaatg      240
ttggaacgga tgacaaatca ttccttcttc tgtttccttg atgggtattc cggatatcat      300
caaattccca tccgtccaga ggaccagagt aagactacgt tcacatgtcc atatggcacc      360
tatgcgtatc gtaggatgtc cttcggactg tgcaacgctc ctgcatcttt ccaaaggtgt      420
atgttgtcta ttttctcggg catgatcgaa gatatcatga aagtcttcat ggatgacttc      480
tcagtttatg gaaagacttt cggtcattgt ctgtagaatc tagacaaagt cttacaacga      540
tgccaagaaa atgacctagt gtttaattgg gaaaagtgcc attttatggg ccgtgaaggg      600
atagttcttg ggcacgagt atccgaatga ggaatcgaag ttgatcgtgc taaaatcgat      660
gttatagatc aaattcgctc tcctgcgaat atcaaaggaa tccgcagctt cttgggacat      720
gccggctttt atagaagggt cctcaaggac ttcacaaaag tt                                762

```

<210> 55

<211> 254

<212> PRT

<213> Oryza sativa

<400> 55

```

Val Arg Lys Glu Val Phe Lys Leu Leu His Ala Gly Ile Ile Tyr Thr
 1              5              10              15
Val Pro Cys Ser Glu Trp Val Ser Thr Val Gln Val Gly Pro Lys Met
      20              25              30
Gly Glx Met Thr Val Val Ala Asn Ala Gln Asn Lys Leu Ile Pro Gln
      35              40              45
Pro Thr Ile Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
      50              55              60
Lys Ala Thr Lys Glu Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met
      65              70              75              80
Leu Glu Arg Met Thr Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr
      85              90              95
Ser Gly Tyr His Gln Ile Pro Ile Arg Pro Glu Asp Gln Ser Lys Thr
      100              105              110
Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr Arg Arg Met Ser Phe
      115              120              125
Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Leu Ser Ile
      130              135              140
Phe Ser Asp Met Ile Glu Asp Ile Met Lys Val Phe Met Asp Asp Phe
      145              150              155              160
Ser Val Tyr Gly Lys Thr Phe Gly His Cys Leu Glx Asn Leu Asp Lys
      165              170              175
Val Leu Gln Arg Cys Gln Glu Asn Asp Leu Val Phe Asn Trp Glu Lys
      180              185              190
Cys His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Arg Val Ser
      195              200              205
Glu Glx Gly Ile Glu Val Asp Arg Ala Lys Ile Asp Val Ile Asp Gln
      210              215              220
Ile Arg Pro Pro Ala Asn Ile Lys Gly Ile Arg Ser Phe Leu Gly His
      225              230              235              240
Ala Gly Phe Tyr Arg Arg Phe Leu Lys Asp Phe Thr Lys Val
      245              250

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<210> 56
 <211> 762
 <212> DNA
 <213> *Oryza sativa*

<400> 56
 gtgcgtaagg aggtcttgaa gctcttgcac gccgagatta tttatcccgt accatataga 60
 gagtgggtta gcccgggtcta gggttatgccg aagaagggac gaatgacggg cattgcaaatt 120
 gctcaaaatg aacttattcc gcaacgaaca gtaaccggat ggaggatgtg catagattac 180
 atgaaactta acaaggctac gaaaaaggat catttcccac tacccttcat tgatgaaatg 240
 ttggaacggc tggcaaatca ttctttcttc cgtttccttg atgggtattc taggtatgat 300
 caaattccca tccatccgga ggaccaaaagt aagactacgt tcacatgttc gtatgatacc 360
 tatgcttata gtaggatgtc cttcggactg tgcaacgctc ctgcatcttt ccaaagggtg 420
 atgatgtcta ttttctccga catgattaag gacattatgg aagtcttcat gcatgacttc 480
 tctatttatg gaaagacctc cggtcattgt ctacaaaatt tagacaaaat ttgcaacga 540
 tgccaagaga aggacctggg acttaattgg gaaaagtgtc atttcatggg ccgatgaagg 600
 atagttctta gtcacgaggt gtccgaataa ggaatcgaag ttgatcgtgc taaaaactat 660
 gtaatagatt agcttccttc tcctgtgaac attaagggga tccgcaattt tttgggacat 720
 gctggctttt atagaagggt catcaaaagc ttcacaaagg tt 762

<210> 57
 <211> 254
 <212> PRT
 <213> *Oryza sativa*

<400> 57
 Val Arg Lys Glu Val Leu Lys Leu Leu His Ala Glu Ile Ile Tyr Pro
 1 5 10 15
 Val Pro Tyr Arg Glu Trp Val Ser Pro Val Glx Val Met Pro Lys Lys
 20 25 30
 Gly Arg Met Thr Val Ile Ala Asn Ala Gln Asn Glu Leu Ile Pro Gln
 35 40 45
 Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Met Lys Leu Asn
 50 55 60
 Lys Ala Thr Lys Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met
 65 70 75 80
 Leu Glu Arg Leu Ala Asn His Ser Phe Phe Arg Phe Leu Asp Gly Tyr
 85 90 95
 Ser Arg Tyr Asp Gln Ile Pro Ile His Pro Glu Asp Gln Ser Lys Thr
 100 105 110
 Thr Phe Thr Cys Ser Tyr Asp Thr Tyr Ala Tyr Arg Arg Met Ser Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile
 130 135 140
 Phe Ser Asp Met Ile Lys Asp Ile Met Glu Val Phe Met His Asp Phe
 145 150 155 160
 Ser Ile Tyr Gly Lys Thr Ser Gly His Cys Leu Gln Asn Leu Asp Lys
 165 170 175
 Ile Leu Gln Arg Cys Gln Glu Lys Asp Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Arg Glu Gly Ile Val Leu Ser His Arg Val Ser
 195 200 205
 Glu Glx Gly Ile Glu Val Asp Arg Ala Lys Asn Tyr Val Ile Asp Glx
 210 215 220
 Leu Pro Ser Pro Val Asn Ile Lys Gly Ile Arg Asn Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val

245

250

<210> 58
 <211> 762
 <212> DNA
 <213> Hordeum vulgare

<400> 58
 gtgcgcaagg aggttttagaa gttcctggaa gcaggatatca tctatcgtgt tgctcatagt 60
 gattgggtga gtcgggtgca ttgtgtccct aagaagggag gcattaccgt tgtccctaata 120
 gataaggatg aattgatccc acagaggact attactggct ataggatggg gattgatttt 180
 aggaaattga ataaagccac taggaaagat cattaccctt tgccttttat cgaccaaagt 240
 cgagaaaggc tgtctaaaca cacacacttc tgcttttctaa acggttattt tggtttctcc 300
 caaataccag ttgcacaatc tgatcaggag aaaaccactt tcacctgccc ttttggtaca 360
 tttgcttata gacgtatgac ttttggctta tgtaatgcac ctgcctcctt tcaaagatgt 420
 atgatggcta tattccctga cttttgtgaa aagattgttg aggttttcat ggatgacttc 480
 tccatttacg gatcttcctt tgatgattgc ctcagcaacc ttgatcgagt cttgcagaga 540
 tgtaaagaca ccaatctttt cttgaattgg aagaagtgcc actttatggg taatgacggc 600
 atcgtcttag gacataaatt ttctgaaaga ggtattgaag tcgataaggc taagggtgat 660
 ggaatcgaga aaatgccata cccacagat atcaaaggga taagaagttt ccttggtcat 720
 gctggtttct atagaagggt cataaaaagac ttcactaagg tt 762

<210> 59
 <211> 254
 <212> PRT
 <213> Hordeum vulgare

<400> 59
 Val Arg Lys Glu Val Glx Lys Phe Leu Glu Ala Gly Ile Ile Tyr Arg
 1 5 10 15
 Val Ala His Ser Asp Trp Leu Ser Arg Val His Cys Val Pro Lys Lys
 20 25 30
 Gly Gly Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln
 35 40 45
 Arg Thr Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn
 50 55 60
 Lys Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met
 65 70 75 80
 Arg Glu Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asn Gly Tyr
 85 90 95
 Phe Gly Phe Ser Gln Ile Pro Val Ala Gln Ser Asp Gln Glu Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Thr Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ala Ile
 130 135 140
 Phe Pro Asp Phe Cys Glu Lys Ile Val Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Ile Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg
 165 170 175
 Val Leu Gln Arg Cys Lys Asp Thr Asn Leu Phe Leu Asn Trp Lys Lys
 180 185 190
 Cys His Phe Met Val Asn Asp Gly Ile Val Leu Gly His Lys Phe Ser
 195 200 205
 Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Gly Ile Glu Lys
 210 215 220
 Met Pro Tyr Pro Thr Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His

225 230 235 240
Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

```
<210> 60
<211> 762
<212> DNA
<213> Hordeum vulgare
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<400> 60						
gtgcgtaaag	aggtcctaaa	gttcctggaa	gcggggtatta	tctatcctgt	tgctcacaac	60
gattgggtga	gtccggtgca	ttgcgtccct	aagaagggat	gcattaccgt	tgtccctaata	120
gataaggatg	aattgatccc	acataggatt	attactggct	ataggatggt	gatcgatttt	180
aggaaaatga	ataaagccac	taggaaagaa	cattaccctt	tgccttttag	cgaccaaata	240
ctagaaaggt	tgtctaaaca	cacacacttc	tgctttctag	acggttattc	tagtttctcc	300
caaatactag	ttgcacaatc	tgatcaggag	aaaaccactt	tcacctacc	gttcggtacc	360
tttgcttata	gacgtatgcc	ttttggctta	tgtaatgcac	ctgccacctt	tcaaagatgt	420
atgatggcta	tattctctga	cttttgtgaa	aagtttgtcg	aggttttcat	ggatgacttt	480
tccgtttacg	gatcttcctt	tgatgattgc	ctcaacaacc	ttgatcgggt	cttgagaga	540
tgtaaagata	ctaactctgt	cttgaaattg	gagaagtgcc	actttatggt	taatgaaggc	600
atcgctcttag	gacataaaaat	ttccgaaaga	ggtattgaat	tcgaataaggc	taagggttgg	660
gcaatcaaga	aaatgccata	ccccagaat	atcaaaagta	taagaagttt	cttgggtccat	720
gctggtttct	atagaaggtt	catcaaggac	tttacaagg	tt		762

```
<210> 61
<211> 254
<212> PRT
<213> Hordeum vulgare
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<400> 61															
Val	Arg	Lys	Glu	Val	Leu	Lys	Phe	Leu	Glu	Ala	Gly	Ile	Ile	Tyr	Pro
1				5					10					15	
Val	Ala	His	Asn	Asp	Trp	Val	Ser	Pro	Val	His	Cys	Val	Pro	Lys	Lys
			20					25					30		
Gly	Cys	Ile	Thr	Val	Val	Pro	Asn	Asp	Lys	Asp	Glu	Leu	Ile	Pro	His
		35					40					45			
Arg	Ile	Ile	Thr	Gly	Tyr	Arg	Met	Val	Ile	Asp	Phe	Arg	Lys	Met	Asn
	50					55					60				
Lys	Ala	Thr	Arg	Lys	Glu	His	Tyr	Pro	Leu	Pro	Phe	Ser	Asp	Gln	Met
65					70					75					80
Leu	Glu	Arg	Leu	Ser	Lys	His	Thr	His	Phe	Cys	Phe	Leu	Asp	Gly	Tyr
				85					90					95	
Ser	Ser	Phe	Ser	Gln	Ile	Leu	Val	Ala	Gln	Ser	Asp	Gln	Glu	Lys	Thr
			100					105					110		
Thr	Phe	Thr	Tyr	Pro	Phe	Gly	Thr	Phe	Ala	Tyr	Arg	Arg	Met	Pro	Phe
		115					120					125			
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Cys	Met	Met	Ala	Ile
	130					135					140				
Phe	Ser	Asp	Phe	Cys	Glu	Lys	Phe	Val	Glu	Val	Phe	Met	Asp	Asp	Phe
145				150						155				160	
Ser	Val	Tyr	Gly	Ser	Ser	Phe	Asp	Asp	Cys	Leu	Asn	Asn	Leu	Asp	Arg
				165					170					175	
Val	Leu	Gln	Arg	Cys	Lys	Asp	Thr	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys
			180					185					190		
Cys	His	Phe	Met	Val	Asn	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Ile	Ser
		195					200					205			
Glu	Arg	Gly	Ile	Glu	Phe	Asp	Lys	Ala	Lys	Val	Gly	Ala	Ile	Lys	Lys

210		215		220
Met Pro Tyr Pro Thr Asp	Ile Lys Gly Ile Arg	Ser Phe Leu Val His		
225	230	235	240	
Ala Gly Phe Tyr Arg Arg	Phe Ile Lys Asp Phe	Thr Lys Val		
	245	250		

<210> 62
 <211> 757
 <212> DNA
 <213> Hordeum vulgare

<400> 62

gaaaagaggt	tgtgaagctc	ctggatgaag	gtattatcta	tcatgttgct	catagcgatt	60
gggtgagtc	ggtgcatagc	gttcctaaga	agggagggcat	taccgttgct	cctaatagata	120
aggatgaatt	gatcccgag	aggattatca	ctggctatag	gatgggtgatc	gatttcagga	180
aactgaataa	agccactagg	aaagatcatt	accctttgcc	ttttatcgac	catatgctag	240
aaaggttgct	caaactcaca	cacttctgct	ttctagacgg	ttattctagt	ttctcccaa	300
taccagttgc	acaatctgat	caggagaaaa	ccactttcac	ctgccctttc	ggtacctttg	360
cttatagacg	tatgcctttt	ggcttatgta	atgcacctgc	cacctttcaa	agatgtatga	420
tggctatatt	ctctaacttt	tgtgaaaata	ttgtcgaggt	tttcatggat	gacttttccg	480
tttacgggtc	ttcttttgat	gattgcctca	gcaaccttga	tcgagtctta	cagagatgta	540
aagacaccaa	tcttgtcttg	aatggggaga	agtgccactt	tatgggttaat	gaaggcatcg	600
tcttaggaca	taaaatttct	gaaagaggta	ttgaagtcga	taaggctaag	gttgatgcaa	660
tcgacaaaat	gccatacccc	acagatatca	aaggtataag	aagtttcctt	ggtcatgggtg	720
gtttctatag	aaggtttatc	aaagatttca	caaaggt			757

<210> 63
 <211> 251
 <212> PRT
 <213> Hordeum vulgare

<400> 63

Lys Glu Val Val Lys Leu Leu Asp Glu Gly Ile Ile Tyr His Val Ala	
1 5 10 15	
His Ser Asp Trp Val Ser Pro Val His Ser Val Pro Lys Lys Gly Gly	
20 25 30	
Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln Arg Ile	
35 40 45	
Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn Lys Ala	
50 55 60	
Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Ile Asp His Met Leu Glu	
65 70 75 80	
Arg Leu Ser Lys Leu Thr His Phe Cys Phe Leu Asp Gly Tyr Ser Ser	
85 90 95	
Phe Ser Gln Ile Pro Val Ala Gln Ser Asp Gln Glu Lys Thr Thr Phe	
100 105 110	
Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Pro Phe Gly Leu	
115 120 125	
Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile Phe Ser	
130 135 140	
Asn Phe Cys Glu Asn Ile Val Glu Val Phe Met Asp Asp Phe Ser Val	
145 150 155 160	
Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg Val Leu	
165 170 175	
Gln Arg Cys Lys Asp Thr Asn Leu Val Leu Asn Gly Glu Lys Cys His	
180 185 190	
Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser Glu Arg	

195	200	205
Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Ile Asp Lys Met Pro		
210	215	220
Tyr Pro Thr Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His Gly Gly		
225	230	235
Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys		240
245	250	

<210> 64

<211> 740

<212> DNA

<213> Hordeum vulgare

<400> 64

gtgcgtaaag	agggtgattaa	attcctagaa	gaagggtatta	tctatcctgt	tgctcacagc	60
gattgggtga	gtccgggtgca	ttgcattcct	aagaaaggag	gcattaccgt	tgccctaata	120
gataaggatg	aattgatccc	atagaggatt	attactggct	ataggatggg	gattgatttt	180
aggaagttga	ataaagccac	taggaaagat	cattaccctt	tgccctttat	cgaccaaata	240
ctagaaaggc	tgtctaaaca	cacacacttc	ttgtttctgg	acggttatac	tggtttctcc	300
caaataccag	ttgcacaatt	tgatcaggag	aaaaccactt	taacctgaca	tttcgggtacc	360
tttgcttata	tacgtatgcc	ttttggcttg	tgtaatgcac	ctgccacctt	tcaaagatgt	420
atgatggcta	tattctccga	cttctgtgaa	aagattgtca	atgttttcat	ggataacttc	480
tccgtttacg	gggtttcctt	tgatgattgc	ctcaacaacg	ttgatcgagt	cttacagaga	540
tgtaaggaca	ccaatgttgt	cttgaattgg	gagaagtgtc	actttatggg	taatgaaggc	600
atcgtcttag	gacataagat	ttctgaaaaga	ggattataag	ttgataaggc	taagggtgat	660
gcaatcgaga	aaatgccata	tccacagata	tcaaagggtat	aagaagtttc	cttggtcatg	720
ctggtttcta	tagaagggttc					740

<210> 65

<211> 247

<212> PRT

<213> Hordeum vulgare

<400> 65

Val Arg Lys Glu Val Ile Lys Phe Leu Glu Glu Gly Ile Ile Tyr Pro	
1 5 10 15	
Val Ala His Ser Asp Trp Val Ser Pro Val His Cys Ile Pro Lys Lys	
20 25 30	
Gly Gly Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Glx	
35 40 45	
Arg Ile Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn	
50 55 60	
Lys Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met	
65 70 75 80	
Leu Glu Arg Leu Ser Lys His Thr His Phe Leu Phe Leu Asp Gly Tyr	
85 90 95	
Thr Gly Phe Ser Gln Ile Pro Val Ala Gln Phe Asp Gln Glu Lys Thr	
100 105 110	
Thr Leu Thr Glx His Phe Gly Thr Phe Ala Tyr Ile Arg Met Pro Phe	
115 120 125	
Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile	
130 135 140	
Phe Ser Asp Phe Cys Glu Lys Ile Val Asn Val Phe Met Asp Asn Phe	
145 150 155 160	
Ser Val Tyr Gly Cys Ser Phe Asp Asp Cys Leu Asn Asn Val Asp Arg	
165 170 175	
Val Leu Gln Arg Cys Lys Asp Thr Asn Val Val Leu Asn Trp Glu Lys	

	180		185		190										
Cys	His	Phe	Met	Val	Asn	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Ile	Ser
	195						200					205			
Glu	Arg	Gly	Ile	Lys	Val	Asp	Lys	Ala	Lys	Val	Asp	Ala	Ile	Glu	Lys
	210					215					220				
Met	Pro	Tyr	Pro	Thr	Asp	Ile	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His
225					230					235					240
Ala	Gly	Phe	Tyr	Arg	Arg	Phe									
				245											

<210> 66
 <211> 762
 <212> DNA
 <213> Avena sativa

<400> 66

gtgCGaaaagg	agggttttcaa	gctcatggat	gctgggtatta	tttaccctat	tgctgatagt	60
gaatgggtta	gtcatgttca	ttgtgttcct	aaaaagggag	gtattaccgt	tgtcccta	120
gataatgatg	agcttattcc	tcaaagaata	gtggtaggct	ataggatgtg	catcgatttt	180
aggaaagtca	ataaagttac	taagaaagat	cactaccgcg	ttccttttat	tgatcaa	240
ttggaaagat	tttctaaaaa	gacccatttt	tgttttcttg	atgggttattc	tggtttctct	300
caaattgttg	ttaaacaaca	agatcaagaa	aaaactactt	ttacttgccc	ttatggaact	360
tatgcttata	gatgtatgcc	tttttggtta	tgtaatgctc	cttctacttt	cctaaggtgc	420
atgtctgcta	tctttcatgg	tttttgtgag	gaaattgtag	aagtgttcat	ggacgacttt	480
tctgtctacg	gaacttcttt	tgataattgt	ctgcacaacc	ttgataaagt	ttacagaga	540
tgtgaaggaa	ctaattcttg	tcttaattgg	gagaaatgcc	acttcatggg	taatgaagg	600
attgttcttg	ggcataaaagt	ttctaaaaaga	ggcatagaag	ttgatagagc	taagggtgag	660
gcaattgaga	agatgccatg	tccaagagac	atcaaaggta	ttcgtagtat	ccttggtcat	720
gctgggtttct	ataggagggtt	catcaaagac	ttcacaaagg	tt		762

<210> 67
 <211> 254
 <212> PRT
 <213> Avena sativa

<400> 67

Val	Arg	Lys	Glu	Val	Phe	Lys	Leu	Met	Asp	Ala	Gly	Ile	Ile	Tyr	Pro
1				5					10					15	
Ile	Ala	Asp	Ser	Glu	Trp	Val	Ser	His	Val	His	Cys	Val	Pro	Lys	Lys
		20						25					30		
Gly	Gly	Ile	Thr	Val	Val	Pro	Asn	Asp	Asn	Asp	Glu	Leu	Ile	Pro	Gln
		35					40					45			
Arg	Ile	Val	Val	Gly	Tyr	Arg	Met	Cys	Ile	Asp	Phe	Arg	Lys	Val	Asn
	50					55					60				
Lys	Val	Thr	Lys	Lys	Asp	His	Tyr	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met
65					70					75				80	
Leu	Glu	Arg	Phe	Ser	Lys	Lys	Thr	His	Phe	Cys	Phe	Leu	Asp	Gly	Tyr
			85						90					95	
Ser	Gly	Phe	Ser	Gln	Ile	Val	Val	Lys	Gln	Gln	Asp	Gln	Glu	Lys	Thr
		100						105				110			
Thr	Phe	Thr	Cys	Pro	Tyr	Gly	Thr	Tyr	Ala	Tyr	Arg	Cys	Met	Pro	Phe
	115					120					125				
Gly	Leu	Cys	Asn	Ala	Pro	Ser	Thr	Phe	Leu	Arg	Cys	Met	Ser	Ala	Ile
	130					135					140				
Phe	His	Gly	Phe	Cys	Glu	Glu	Ile	Val	Glu	Val	Phe	Met	Asp	Asp	Phe
145					150					155					160
Ser	Val	Tyr	Gly	Thr	Ser	Phe	Asp	Asn	Cys	Leu	His	Asn	Leu	Asp	Lys

				165					170					175		
Val	Leu	Gln	Arg	Cys	Glu	Gly	Thr	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys	
			180					185					190			
Cys	His	Phe	Met	Val	Asn	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Val	Ser	
		195					200					205				
Lys	Arg	Gly	Ile	Glu	Val	Asp	Arg	Ala	Lys	Val	Glu	Ala	Ile	Glu	Lys	
	210					215					220					
Met	Pro	Cys	Pro	Arg	Asp	Ile	Lys	Gly	Ile	Arg	Ser	Ile	Leu	Gly	His	
225					230					235					240	
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val			
				245					250							

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<210> 68
<211> 762
<212> DNA
<213> Avena sativa
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<400> 68						
gtgcgcaaag	aggctctttaa	gttccttggat	gctgggtatta	tttaccctat	tgctgatagt	60
caatgggtta	gccttggttca	ttgtgtcccc	aagaaagggg	gaataactgt	tgtgcctaata	120
gaagataatg	agcttataacc	ccaaagagta	gtgggttggt	atagaatgtg	cattgattttt	180
agaaggatta	ataaagttag	taggaaagat	cattatcctt	tgccctttat	tgatcaaata	240
cttgagaggt	tgtccaaaaa	gactcacttt	tgttttcttg	atgggtcattc	tgggttttct	300
caaatgtgtg	tgaaagcaca	agaccaagag	aaaactactt	tcacttggtcc	ttatggtact	360
tatgattata	ggcgtatgcc	ttttggttta	tgtaatgctc	ctgctacctt	tcagagatgt	420
atgtctgcta	tattttcatgg	tttttgtaga	gaaattgtgg	agggttttcat	ggacgattttt	480
tctgtctatg	gaacttcttt	tgataactgt	ttgcacaacc	ttgataaatt	tttgtagaga	540
tttgaagaaa	ccaaccttgt	tcttaattgg	gagaaatgcc	atttcattggt	taatgaaggg	600
attgttcttg	gacacagaat	ctcagaaaag	ggcattgaag	ttgacagagc	caaaattgaa	660
gcaatttgga	acatgccttg	ccctagagat	attaaaggta	ttcgtagtat	ccttgggtcat	720
gctggtttct	atagtagggt	catcaaaagc	tttacaaaag	tt		762

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<210> 69
<211> 254
<212> PRT
<213> Avena sativa
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<400> 69															
Val	Arg	Lys	Glu	Val	Phe	Lys	Phe	Leu	Asp	Ala	Gly	Ile	Ile	Tyr	Pro
1				5					10					15	
Ile	Ala	Asp	Ser	Gln	Trp	Val	Ser	Leu	Val	His	Cys	Val	Pro	Lys	Lys
			20					25					30		
Gly	Gly	Ile	Thr	Val	Val	Pro	Asn	Glu	Asp	Asn	Glu	Leu	Ile	Pro	Gln
		35					40					45			
Arg	Val	Val	Val	Val	Tyr	Arg	Met	Cys	Ile	Asp	Phe	Arg	Arg	Ile	Asn
	50					55					60				
Lys	Val	Thr	Arg	Lys	Asp	His	Tyr	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met
65					70					75					80
Leu	Glu	Arg	Leu	Ser	Lys	Lys	Thr	His	Phe	Cys	Phe	Leu	Asp	Gly	His
				85					90					95	
Ser	Gly	Phe	Ser	Gln	Ile	Val	Val	Lys	Ala	Gln	Asp	Gln	Glu	Lys	Thr
			100					105					110		
Thr	Phe	Thr	Cys	Pro	Tyr	Gly	Thr	Tyr	Asp	Tyr	Arg	Arg	Met	Pro	Phe
		115					120					125			
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Cys	Met	Ser	Ala	Ile
	130					135					140				
Phe	His	Gly	Phe	Cys	Glu	Glu	Ile	Val	Glu	Val	Phe	Met	Asp	Asp	Phe

145		150		155		160									
Ser	Val	Tyr	Gly	Thr	Ser	Phe	Asp	Asn	Cys	Leu	His	Asn	Leu	Asp	Lys
				165					170					175	
Phe	Leu	Gln	Arg	Phe	Glu	Glu	Thr	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys
			180					185					190		
Cys	His	Phe	Met	Val	Asn	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Ile	Ser
		195					200					205			
Glu	Arg	Gly	Ile	Glu	Val	Asp	Arg	Ala	Lys	Ile	Glu	Ala	Ile	Glu	Asn
		210				215					220				
Met	Pro	Cys	Pro	Arg	Asp	Ile	Lys	Gly	Ile	Arg	Ser	Ile	Leu	Gly	His
225					230					235				240	
Ala	Gly	Phe	Tyr	Ser	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
				245					250						

<210> 70
 <211> 756
 <212> DNA
 <213> Avena sativa

<400> 70																	
aaggagggttt	ttaaactcct	tgatgttggt	attattttacc	ctattgctga	tagtgaatgg												60
gtagtcttg	ttcattgtgt	tcctaaaaag	ggaggtatta	ccgttggtcc	taatgataat												120
gatgagctta	ttcctcaaag	aatagtggta	ggctatagga	tgtgcataga	ttttaggaaa												180
gttaataaag	ttactaagaa	agatcactac	ccgcttcctt	ttattgatca	aatggttgaa												240
aggttggtcta	aaaagaccca	tttttggttt	cttgatggtt	actctagctt	ctctcaaatt												300
gctgttaaac	aacaagatca	agaaaaaact	acttttactt	gcccttatgg	aacttttgct												360
tatagacgta	tgctattgg	tttatgtaat	gctcctgcta	cttttcaaag	gtgtatgtct												420
gctatatattc	atgggttttg	tgaggaaaatt	gtagaagtgt	tcattggatga	cttttctgtc												480
tatggaactt	cttttgataa	ttgcctgcac	aaccttgata	aagttttgca	gagatgtgaa												540
gaaactaata	ttgttcttaa	ttgggagaaa	ttccacttca	tgggttaatga	agggattgtc												600
cttgggcata	aagtttctaa	aagaggcata	gaagttgata	gagctaaggt	tgaggcaatt												660
gagaagatgc	catgcccaag	agacatcaaa	ggtatacgta	gtatccttgg	tcattgctgg												720
ttctatagaa	ggtttatcaa	agacttcaca	aagggtt														756

<210> 71
 <211> 252
 <212> PRT
 <213> Avena sativa

<400> 71																	
Lys	Glu	Val	Phe	Lys	Leu	Leu	Asp	Val	Gly	Ile	Ile	Tyr	Pro	Ile	Ala		
1				5					10					15			
Asp	Ser	Glu	Trp	Val	Ser	Leu	Val	His	Cys	Val	Pro	Lys	Lys	Gly	Gly		
			20					25					30				
Ile	Thr	Val	Val	Pro	Asn	Asp	Asn	Asp	Glu	Leu	Ile	Pro	Gln	Arg	Ile		
			35				40					45					
Val	Val	Gly	Tyr	Arg	Met	Cys	Ile	Asp	Phe	Arg	Lys	Val	Asn	Lys	Val		
			50			55					60						
Thr	Lys	Lys	Asp	His	Tyr	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met	Leu	Glu		
65					70					75				80			
Arg	Leu	Ser	Lys	Lys	Thr	His	Phe	Cys	Phe	Leu	Asp	Gly	Tyr	Ser	Ser		
			85					90					95				
Phe	Ser	Gln	Ile	Ala	Val	Lys	Gln	Gln	Asp	Gln	Glu	Lys	Thr	Thr	Phe		
			100				105						110				
Thr	Cys	Pro	Tyr	Gly	Thr	Phe	Ala	Tyr	Arg	Arg	Met	Pro	Ile	Gly	Leu		
		115					120					125					
Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Cys	Met	Ser	Ala	Ile	Phe	His		

130		135		140
Gly Phe Cys Glu Glu Ile Val Glu Val Phe Met Asp Asp Phe Ser Val				
145		150		155
Tyr Gly Thr Ser Phe Asp Asn Cys Leu His Asn Leu Asp Lys Val Leu				
	165		170	175
Gln Arg Cys Glu Glu Thr Asn Ile Val Leu Asn Trp Glu Lys Phe His				
	180		185	190
Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser Lys Arg				
	195		200	205
Gly Ile Glu Val Asp Arg Ala Lys Val Glu Ala Ile Glu Lys Met Pro				
	210		215	220
Cys Pro Arg Asp Ile Lys Gly Ile Arg Ser Ile Leu Gly His Ala Gly				
225		230		235
Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val				240
	245		250	

<210> 72

<211> 748

<212> DNA

<213> Secale cereale

<400> 72

gtgcggaaag aggtcttttaa actcctagag gcagggtatta actatcccat tgctgatagc	60
cagcgggtaa gtcattgtcca ttgtgttcct aagaaaggag gtatgactgt cgtccctaag	120
gataaagatg aatttatccc gcaaagaata gttacagggt ataggatggg aattgatttt	180
cgtaagttaa ataaagctac tatgaaagat cattaccct tgccatttat tgatcaaagtg	240
ccagacaggt tatccaaaca tactcatttc tgctttctag atgggtatttc tgggtttctct	300
caaatacctt tgtcaaaggg ggatcaagaa aagaccacct ttacttgtcc tttcgggtacc	360
tttgcttata gaggtatgcc ttttggttta tgtaatgcac ctgctacctt tcaaagatgt	420
atgatcgtaa tattctctgt cttttttgaa aagattgttg aggtattcat ggatgatttc	480
tccgtttatg gaacttcttt tgatgattgc ttaagcaacc ttgatcgagt tttgcagaga	540
tgtgaagata ctaaccttgt cttgaattgg gagaagtgcc actttatggg taatgaaggc	600
attttcttgg gacataaaat ttctgaaaga ggtactgaag ttgagaaagc taaagtggat	660
gctattgaaa agatgccatg ccctaaggat atgaaaggta tacgaagttt ccttggtcac	720
gctgggtttt ataggagggt cataaaag	748

<210> 73

<211> 249

<212> PRT

<213> Secale cereale

<400> 73

Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Ile Asn Tyr Pro	
1	15
Ile Ala Asp Ser Gln Arg Val Ser His Val His Cys Val Pro Lys Lys	
	30
Gly Gly Met Thr Val Val Pro Lys Asp Lys Asp Glu Phe Ile Pro Gln	
	45
Arg Ile Val Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn	
	60
Lys Ala Thr Met Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met	
65	80
Pro Asp Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asp Gly Tyr	
	95
Ser Gly Phe Ser Gln Ile Pro Leu Ser Lys Gly Asp Gln Glu Lys Thr	
	110
Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Gly Met Pro Phe	

115 120 125
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Ile Val Ile
 130 135 140
 Phe Ser Val Phe Phe Glu Lys Ile Val Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Tyr Gly Thr Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg
 165 170 175
 Val Leu Gln Arg Cys Glu Asp Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Asn Glu Gly Ile Phe Leu Gly His Lys Ile Ser
 195 200 205
 Glu Arg Gly Thr Glu Val Glu Lys Ala Lys Val Asp Ala Ile Glu Lys
 210 215 220
 Met Pro Cys Pro Lys Asp Met Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys
 245

<210> 74

<211> 762

<212> DNA

<213> Secale cereale

<400> 74

gtgcggaagg	aggtcgttaa	gcttccagag	gcaggtatta	tctatcccgt	tgctgatagc	60
cagtgggtaa	gtcatgtcca	ttgtgtccct	aagaaggagg	gtatgactgt	cgttccta	120
gacaaacatg	aattgatccc	gcaaagaata	gttacagggt	ataggatggt	aattgatttc	180
cgtaagttaa	ataaagctac	taagaaagat	cattaccctt	tgccatttat	tgatcaaatg	240
ctagacaggt	tatccaaaca	tactcatttt	tgctttctag	atggttatta	tggtttctct	300
caaatacctg	tgtcaaaagg	ggatcaagaa	aagaccactt	tcacttgtcc	tttcgggtacc	360
tttgcttata	gacgtatgcc	ttttgggtta	tgtaatgcac	ctgctacctt	tcaaagatgt	420
atgatggcta	tattatctga	tttttgagaa	aagattgttg	aggttttcat	ggatgatttc	480
tccgtttacg	gaacttcttt	tgatgactac	ttaagcaaca	atgatcgagt	tttgagaga	540
tgtgaagaca	ctaactttgt	tttgaattgg	gagaagtgcc	actttatggg	taatgaaggc	600
attgtcttgg	gacaaaaaat	ttctgaaaaga	ggatttgaag	ttgacaaagc	taaagtcgat	660
gctgttgaaa	agatgccatg	cccccaaggac	atcaaaggta	tacgaagttt	ccttggtcat	720
gttgggtttt	ataggagggtt	catcaaagac	ttcacgaaag	tt		762

<210> 75

<211> 254

<212> PRT

<213> Secale cereale

<400> 75

Val Arg Lys Glu Val Val Lys Leu Pro Glu Ala Gly Ile Ile Tyr Pro	
1 5 10 15	
Val Ala Asp Ser Gln Trp Val Ser His Val His Cys Val Pro Lys Lys	
20 25 30	
Gly Gly Met Thr Val Val Pro Asn Asp Lys His Glu Leu Ile Pro Gln	
35 40 45	
Arg Ile Val Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn	
50 55 60	
Lys Ala Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met	
65 70 75 80	
Leu Asp Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asp Gly Tyr	
85 90 95	
Tyr Gly Phe Ser Gln Ile Pro Val Ser Lys Gly Asp Gln Glu Lys Thr	

100	105	110
Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Pro Phe		
115	120	125
Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile		
130	135	140
Leu Ser Asp Phe Glx Glu Lys Ile Val Glu Val Phe Met Asp Asp Phe		
145	150	155
Ser Val Tyr Gly Thr Ser Phe Asp Asp Tyr Leu Ser Asn Asn Asp Arg		
165	170	175
Val Leu Gln Arg Cys Glu Asp Thr Asn Leu Val Leu Asn Trp Glu Lys		
180	185	190
Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly Gln Lys Ile Ser		
195	200	205
Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Val Glu Lys		
210	215	220
Met Pro Cys Pro Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His		
225	230	235
Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val		
245	250	

<210> 76

<211> 762

<212> DNA

<213> Secale cereale

<400> 76

gtgcgtaagg	agggtggttaa	gctcctagaa	gcaggtatta	tctatccagt	tgctgatagt	60
cagtgggttaa	gtcatgtcca	ttatgttcct	aagaaaggag	gtatgactgt	tgtcccta	120
gataaagatg	aattgatccc	gcaaagaata	gttacagggt	ataggatggt	aagtgatttc	180
cgtaagttga	ataaagccac	taagaaagat	cattaccctt	tgccatttat	tgatcaaagt	240
ctagaaaggt	tatccaaaca	tactcatttc	ttctttctag	atggttattc	tggtttctct	300
caaatacctg	tgtaaaaagg	ggatcaagaa	aagaccacct	ttacttgtac	tttcggtacc	360
tttgcttata	gacgtatgcc	ttttgggtta	tgtaatgcac	ctgctacctt	tcaaagatgc	420
atgatggcta	tattctctga	cttttgtgaa	aagattgttg	aggtattcat	ggatgatttc	480
tccgtttacg	gaacttcttt	tgatgattgc	ttaagcaacc	ttgatcgagt	tttgcagaga	540
tgtgaagaca	ctaaccttgt	cttgaattgc	gagaagtgcc	actttatggt	taatgaaggc	600
attgtcttgg	gacataaaat	ttctgaaata	ggtattgaag	ttgacaaagc	taaagttgat	660
gctattgaaa	agatgccatg	cgcaaaggac	atcaaaggta	tacggagttt	ccttggtcat	720
gccgggtttt	ataggagggt	catcaaagat	ttctcaaagg	tt		762

<210> 77

<211> 254

<212> PRT

<213> Secale cereale

<400> 77

Val Arg Lys Glu Val Val Lys Leu Leu Glu Ala Gly Ile Ile Tyr Pro	
1	15
Val Ala Asp Ser Gln Trp Val Ser His Val His Tyr Val Pro Lys Lys	
20	30
Gly Gly Met Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln	
35	45
Arg Ile Val Thr Gly Tyr Arg Met Val Ser Asp Phe Arg Lys Leu Asn	
50	60
Lys Ala Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met	
65	80
Leu Glu Arg Leu Ser Lys His Thr His Phe Phe Phe Leu Asp Gly Tyr	

				85						90					95				
Ser	Gly	Phe	Ser	Gln	Ile	Pro	Val	Ser	Lys	Gly	Asp	Gln	Glu	Lys	Thr				
			100					105					110						
Thr	Phe	Thr	Cys	Thr	Phe	Gly	Thr	Phe	Ala	Tyr	Arg	Arg	Met	Pro	Phe				
		115					120					125							
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Cys	Met	Met	Ala	Ile				
	130					135					140								
Phe	Ser	Asp	Phe	Cys	Glu	Lys	Ile	Val	Glu	Val	Phe	Met	Asp	Asp	Phe				
145					150					155					160				
Ser	Val	Tyr	Gly	Thr	Ser	Phe	Asp	Asp	Cys	Leu	Ser	Asn	Leu	Asp	Arg				
				165					170					175					
Val	Leu	Gln	Arg	Cys	Glu	Asp	Thr	Asn	Leu	Val	Leu	Asn	Cys	Glu	Lys				
			180					185					190						
Cys	His	Phe	Met	Val	Asn	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Ile	Ser				
		195					200					205							
Glu	Ile	Gly	Ile	Glu	Val	Asp	Lys	Ala	Lys	Val	Asp	Ala	Ile	Glu	Lys				
	210					215					220								
Met	Pro	Cys	Ala	Lys	Asp	Ile	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His				
225					230					235					240				
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Ser	Lys	Val						
				245					250										

<210> 78

<211> 759

<212> DNA

<213> Secale cereale

<400> 78

gtg	cg	ca	aagg	aag	tttt	ta	gttt	ct	agag	gc	ag	gt	ataa	tct	at	cc	ag	tg	ct	ga	tagc	60	
cag	tg	gg	gt	aa	gtc	ct	gt	cca	tt	gt	gc	cc	aaga	ag	gg	gag	gt	at	gc	act	gt	ag	120
gata	aa	gat	g	aatt	gat	ctc	gca	aa	ga	aatt	gtt	ac	ag	gt	t	at	ag	gat	gg	aatt	gat	ttt	180
cgca	aa	tt	aa	ataa	ag	cc	ac	ta	ag	aa	gat	ca	at	ac	cc	tt	tg	cc	tt	tt	at	tg	240
ctag	aa	agg	t	at	cc	aa	ac	ca	cc	ca	tt	tt	tg	ct	tt	ct	ag	tt	tt	ct	ct	ct	300
caa	at	ac	ct	tg	t	ca	aa	ag	gg	ataa	ag	aa	aag	ac	ca	ct	tt	ac	tt	gt	cc	ct	360
ttg	ct	ta	tag	ac	gt	at	gc	ct	ttt	g	gt	tt	at	gt	at	gc	at	gc	tt	tt	ca	ac	420
tgat	gg	ct	at	act	ct	at	gat	tttt	gt	g	aaa	ga	at	gt	tt	gat	gttt	tt	cat	gg	at	ga	480
tatt	ta	cg	aa	act	tt	ct	tt	tg	at	ga	tt	gc	tt	gat	cg	ag	tt	tg	ca	ga	gat	g	540
tga	ag	aa	act	aat	ct	tg	ct	tga	act	gg	ga	aa	ag	tt	ccc	ac	tt	at	gg	tt	at	ga	600
tgct	tg	gg	ac	ata	aa	tt	tc	tga	ag	ag	gt	acc	ga	ag	tt	g	ac	aa	ag	ct	aa	ag	660
gtt	g	aaa	aga	tg	cc	at	gc	ca	ag	ga	cat	ca	ag	gt	ataa	ga	ag	tt	ct	tg	gt	cat	720
ggg	tt	t	tata	gg	ag	gt	tt	at	ca	ag	ga	ct	ac	ca	ag	gt							759

<210> 79

<211> 254

<212> PRT

<213> Secale cereale

<400> 79

Val	Arg	Lys	Glu	Val	Phe	Lys	Phe	Leu	Glu	Ala	Gly	Ile	Ile	Tyr	Pro							
1				5				10						15								
Val	Ala	Asp	Ser	Gln	Trp	Val	Ser	Pro	Val	His	Cys	Val	Pro	Lys	Lys							
		20					25					30										
Gly	Gly	Met	Thr	Val	Val	Pro	Asn	Asp	Lys	Asp	Glu	Leu	Ile	Ser	Gln							
		35				40					45											
Arg	Ile	Val	Thr	Gly	Tyr	Arg	Met	Val	Ile	Asp	Phe	Arg	Lys	Leu	Asn							
	50					55					60											
Lys	Ala	Thr	Lys	Lys	Asp	Gln	Tyr	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met							

65					70					75				80
Leu	Glu	Arg	Leu	Ser	Lys	His	Thr	His	Phe	Cys	Phe	Leu	Asp	Gly Tyr
				85					90					95
Ser	Ser	Phe	Ser	Gln	Ile	Pro	Met	Ser	Lys	Gly	Asp	Lys	Glu	Lys Thr
			100					105					110	
Thr	Phe	Thr	Cys	Pro	Phe	Gly	Thr	Phe	Ala	Tyr	Arg	Arg	Met	Pro Phe
		115					120					125		
Gly	Leu	Cys	Asn	Ala	Ser	Ala	Thr	Phe	Gln	Thr	Cys	Met	Met	Ala Ile
	130					135					140			
Leu	Tyr	Asp	Phe	Cys	Glu	Arg	Ile	Val	Asp	Val	Phe	Met	Asp	Asp Phe
145					150				155					160
Cys	Ile	Tyr	Glu	Thr	Ser	Phe	Asp	Asp	Cys	Leu	Ser	Asn	Leu	Asp Arg
				165					170				175	
Val	Leu	Gln	Arg	Cys	Glu	Glu	Thr	Asn	Leu	Val	Leu	Asn	Trp	Glu Lys
			180					185				190		
Ser	His	Phe	Met	Val	Asn	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Ile Ser
		195					200					205		
Glu	Arg	Gly	Thr	Glu	Val	Asp	Lys	Ala	Lys	Val	Asp	Ala	Val	Glu Lys
	210					215					220			
Met	Pro	Cys	Pro	Lys	Asp	Ile	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly His
225					230					235				240
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val	
				245					250					

<210> 80

<211> 761

<212> DNA

<213> Triticum aestivum

<400> 80

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cagtgggtaa	gtcctgtcca	ttgtgtccct	aagaagggag	gtattactgt	tgccctaata	120
gataaagatg	aattgattcc	tcaaagaatt	attacgggta	taggatggta	attgatttcc	180
gcaaattaaa	taaagccact	aagagagatc	attaccctt	accttttatt	gatcaaattc	240
tagaaagatt	atgcaaacat	acacattatt	gcttccaaga	tggttatcct	ggtttttctc	300
aaatacctgt	gtcggctaaa	gatcaatcaa	agactacttt	tacatgccct	tttggtactt	360
ttgcttatag	atgtatgcct	tttggtttat	gtaatgcacc	tgctaccttt	caaagatgca	420
tgatggctat	attctctgat	ttttgtgaaa	agatttgtga	ggttttcatg	gatgactttt	480
ccgtctatgg	ttcctctttt	gatgattgct	tgagcaatct	tgatcgagtt	ttgcagagat	540
gtgaagaaac	taatcttgct	ttgaattggg	aaaagtgtca	ctttatgggt	aatgaaggta	600
ttgtcttggg	gcacaaagtt	tctgaaagag	gtattgaagt	tgataaagcc	aagggtgaca	660
ctattgaaaa	gataccatgt	cccaaggaca	tcaaaggtag	aagaagtttc	cttggtcacg	720
ccggatttta	taggagggttc	ataaaaagatt	tcacaaagggt	t		761

<210> 81

<211> 254

<212> PRT

<213> Triticum aestivum

<400> 81

Val	Arg	Lys	Glu	Val	Leu	Lys	Phe	Leu	Glu	Val	Gly	Ile	Ile	Tyr	Pro
1				5				10						15	
Val	Ala	Asp	Ser	Gln	Trp	Val	Ser	Pro	Val	His	Cys	Val	Pro	Lys	Lys
			20					25					30		
Gly	Gly	Ile	Thr	Val	Val	Pro	Asn	Asp	Lys	Asp	Glu	Leu	Ile	Pro	Gln
		35				40					45				
Arg	Ile	Ile	Thr	Gly	Tyr	Arg	Met	Val	Ile	Asp	Phe	Arg	Lys	Leu	Asn

50		55		60
Lys Ala Thr Lys Arg Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Ile				
65		70		75
Leu Glu Arg Leu Cys Lys His Thr His Tyr Cys Phe Gln Asp Gly Tyr				80
	85		90	
Pro Gly Phe Ser Gln Ile Pro Val Ser Ala Lys Asp Gln Ser Lys Thr				95
	100		105	110
Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Cys Met Pro Phe				
	115		120	125
Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile				
	130		135	140
Phe Ser Asp Phe Cys Glu Lys Ile Cys Glu Val Phe Met Asp Asp Phe				
145		150		155
Ser Val Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg				160
	165		170	175
Val Leu Gln Arg Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys				
	180		185	190
Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser				
	195		200	205
Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Thr Ile Glu Lys				
	210		215	220
Ile Pro Cys Pro Lys Asp Ile Lys Gly Thr Arg Ser Phe Leu Gly His				
225		230		235
Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val				240
	245		250	

<210> 82

<211> 780

<212> DNA

<213> Triticum aestivum

<400> 82

gtgcggaagg aggtgttttaa gctccttgag gcagggtataa tttatcccgt tgctgatagt	60
aagtgggttaa ttcctgtcca ttaagtgatc gtgattactg ttgttcctaa gaagggaggt	120
attaccgttg ttcctaataga taaagatgaa ttgattcctc aaagaaccat tactggttat	180
aggatggtaa ttgatttccg caaattaaat aaggctacta aaaaatatca ttaccctta	240
ccttttatcg atcaaatgct agaaagatta tccaaacata cacatttttg ctttctagat	300
ggttactctg gtttctctca aatacctgtg tcagccaaaag atcaatcaaa gactactttt	360
acatgccctt ttggtacttt tgcttataga cgtatgcctt ttggtttatg taatgcacct	420
gctacctttc aaagatacat gatggctata ttatctgact tttgtgaaaa gatttgtag	480
gttttcatgg acgactcttc catctatgga tcttcttttg atgattgctt gagcaacctt	540
gacgagttt tgcagagatg tgaagaaact tatcttgtct tgaattggga aaagtgccaa	600
tttatggtta atgaaggat tgccttgggg cataaagttt ctgaaagagg tattcgagtt	660
gataaagcca aggttgatgc tattgaaaag atgccatgtc ccatggacat caaaggtata	720
agaagtttcc ttggtcatgc cggtttttat aggaggttca taaaagactt cacgaaggtt	780

<210> 83

<211> 260

<212> PRT

<213> Triticum aestivum

<400> 83

Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Ile Ile Tyr Pro	
1	5
Val Ala Asp Ser Lys Trp Val Ile Pro Val His Glx Val Ile Val Ile	10
	15
	20
Thr Val Val Pro Lys Lys Gly Gly Ile Thr Val Val Pro Asn Asp Lys	25
	30

35	40	45
Asp Glu Leu Ile Pro Gln Arg Thr Ile Thr Gly Tyr Arg Met Val Ile		
50	55	60
Asp Phe Arg Lys Leu Asn Lys Ala Thr Lys Lys Tyr His Tyr Pro Leu		
65	70	75
Pro Phe Ile Asp Gln Met Leu Glu Arg Leu Ser Lys His Thr His Phe		
85	90	95
Cys Phe Leu Asp Gly Tyr Ser Gly Phe Ser Gln Ile Pro Val Ser Ala		
100	105	110
Lys Asp Gln Ser Lys Thr Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala		
115	120	125
Tyr Arg Arg Met Pro Phe Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln		
130	135	140
Arg Tyr Met Met Ala Ile Leu Ser Asp Phe Cys Glu Lys Ile Cys Glu		
145	150	155
Val Phe Met Asp Asp Ser Ser Ile Tyr Gly Ser Ser Phe Asp Asp Cys		
165	170	175
Leu Ser Asn Leu Asp Arg Val Leu Gln Arg Cys Glu Glu Thr Tyr Leu		
180	185	190
Val Leu Asn Trp Glu Lys Cys Gln Phe Met Val Asn Glu Gly Ile Val		
195	200	205
Leu Gly His Lys Val Ser Glu Arg Gly Ile Arg Val Asp Lys Ala Lys		
210	215	220
Val Asp Ala Ile Glu Lys Met Pro Cys Pro Met Asp Ile Lys Gly Ile		
225	230	235
Arg Ser Phe Leu Gly His Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp		
245	250	255
Phe Thr Lys Val		
260		

<210> 84

<211> 762

<212> DNA

<213> Triticum aestivum

<400> 84

gtgcgtaagg aggtattcaa gcttctggag gcaggtataa tttatcccgt tgttgatagt	60
caatgggtaa gtccgtgtcca ttgtgtcctt aagaagggag gtattactgt tgtcccctaat	120
gataaagatg aattgattcc gcaaagaatt atcacagggt ataggatggg aattgatttc	180
cgtaagttaa ataaagctac taagaaagat cattaccctt taccttttat tgatcaaag	240
ttagaaagat tatgcaaaca tacacattat tgctttctag atgggtattc tggtttctct	300
caaataacctg tgtcagctaa ggatcaatca aagactactt ttacatgccc ttttggtact	360
tttggttata gacgtatgcc tttcgattta tgtaatgcac ctgctacctt tcaaatatgc	420
atgatggcta tattctctga cttttgcgaa aagattttgt aggttttcat ggacgacttt	480
tccgtctatg gttcctctta tgatgattgc ttgagcaatc ttaatcgagt tttgcagaga	540
tgtgaagaaa ctaatcttgt cttgaattgg gaaaagtgcc actttatggg taatgaaggt	600
attgtcttgg ggcacaaagt ttctgaacga ggtattgaag ttgataaggc caaggttgat	660
gctattgaaa agatgacatg tcccaaggac atcaaaggta taagaagttt ccttggtcac	720
gccagatttt ataggagggt cataaaagac ttcacaaagg tt	762

<210> 85

<211> 254

<212> PRT

<213> Triticum aestivum

<400> 85

Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Ile Ile Tyr Pro

1	5	10	15
Val Val Asp Ser Gln Trp Val Ser Pro Val His Cys Val Leu Lys Lys			
	20	25	30
Gly Gly Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln			
	35	40	45
Arg Ile Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn			
	50	55	60
Lys Ala Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met			
65	70	75	80
Leu Glu Arg Leu Cys Lys His Thr His Tyr Cys Phe Leu Asp Gly Tyr			
	85	90	95
Ser Gly Phe Ser Gln Ile Pro Val Ser Ala Lys Asp Gln Ser Lys Thr			
	100	105	110
Thr Phe Thr Cys Pro Phe Gly Thr Phe Gly Tyr Arg Arg Met Pro Phe			
	115	120	125
Asp Leu Cys Asn Ala Pro Ala Thr Phe Gln Ile Cys Met Met Ala Ile			
	130	135	140
Phe Ser Asp Phe Cys Glu Lys Ile Cys Glu Val Phe Met Asp Asp Phe			
145	150	155	160
Ser Val Tyr Gly Ser Ser Tyr Asp Asp Cys Leu Ser Asn Leu Asn Arg			
	165	170	175
Val Leu Gln Arg Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys			
	180	185	190
Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser			
	195	200	205
Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Ile Glu Lys			
	210	215	220
Met Thr Cys Pro Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His			
225	230	235	240
Ala Arg Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val			
	245	250	

<210> 86

<211> 762

<212> DNA

<213> Triticum aestivum

<400> 86

gtgcggaaag aggtgctcaa gcttctggag gcaggtataa tttatcccgt tgctgagagt	60
cagtgggtaa gtcctgtcca ttgtgtccct aagaaggag gtattactgt tgtcccta	120
gataaagatg aattgattcc tcaaagaatt attacaggtt ataggatggg aattgatttc	180
cgcaaattaa ataaagccac caagaaagat cattaccctt taccttttat tgatcaa	240
ctagaaagat tatgcaaaca tacacattat tgcttcctag atgggtattc tgggttctct	300
caaatacctg tgtcgggctaa agatcaatca aagactactt ttacatgccc ttttggtact	360
tttgcttata gacgtatgcc ttttggttta tgtaatgcac cttctacctt tcaaagatgc	420
atgatggcta tatttctctga tttttgtgaa aagatttgtg aggttttcat ggacgaattt	480
tccgtctatg gttcctcttt tgatgattgc ttgagcaatc ctgatcgagt tttgcagaga	540
tgtgaagaaa ctaatcttgt cttgaattgg gaaaagtgcc actttatggg taatgaagg	600
attgtcttgg ggcacaaagt ttctgaaaga ggtattgaag ttgataaagc caaggttgac	660
gctattgaaa agatgccatg tccaaggac atcaaaggta taagaagttt ccttggtcac	720
gccggatttt ataggagggt cataaaagac ttcacaaagg tt	762

<210> 87

<211> 254

<212> PRT

<213> Triticum aestivum

<400> 87

Val	Arg	Lys	Glu	Val	Leu	Lys	Leu	Leu	Glu	Ala	Gly	Ile	Ile	Tyr	Pro
1				5					10					15	
Val	Ala	Glu	Ser	Gln	Trp	Val	Ser	Pro	Val	His	Cys	Val	Pro	Lys	Lys
		20						25					30		
Gly	Gly	Ile	Thr	Val	Val	Pro	Asn	Asp	Lys	Asp	Glu	Leu	Ile	Pro	Gln
		35					40					45			
Arg	Ile	Ile	Thr	Gly	Tyr	Arg	Met	Val	Ile	Asp	Phe	Arg	Lys	Leu	Asn
	50					55					60				
Lys	Ala	Thr	Lys	Lys	Asp	His	Tyr	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met
65					70					75					80
Leu	Glu	Arg	Leu	Cys	Lys	His	Thr	His	Tyr	Cys	Phe	Leu	Asp	Gly	Tyr
			85					90						95	
Ser	Gly	Phe	Ser	Gln	Ile	Pro	Val	Ser	Ala	Lys	Asp	Gln	Ser	Lys	Thr
		100						105					110		
Thr	Phe	Thr	Cys	Pro	Phe	Gly	Thr	Phe	Ala	Tyr	Arg	Arg	Met	Pro	Phe
		115					120					125			
Gly	Leu	Cys	Asn	Ala	Pro	Ser	Thr	Phe	Gln	Arg	Cys	Met	Met	Ala	Ile
	130					135					140				
Phe	Ser	Asp	Phe	Cys	Glu	Lys	Ile	Cys	Glu	Val	Phe	Met	Asp	Glu	Phe
145					150				155						160
Ser	Val	Tyr	Gly	Ser	Ser	Phe	Asp	Asp	Cys	Leu	Ser	Asn	Pro	Asp	Arg
			165					170						175	
Val	Leu	Gln	Arg	Cys	Glu	Glu	Thr	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys
		180						185					190		
Cys	His	Phe	Met	Val	Asn	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Val	Ser
		195					200					205			
Glu	Arg	Gly	Ile	Glu	Val	Asp	Lys	Ala	Lys	Val	Asp	Ala	Ile	Glu	Lys
	210					215					220				
Met	Pro	Cys	Pro	Lys	Asp	Ile	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His
225					230					235					240
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
			245						250						

<210> 88

<211> 762

<212> DNA

<213> Triticum aestivum

<400> 88

gtgcgtaagg	aggttttcaa	gttccttgag	gcaggtatta	cttatcccgt	tgctgatagt	60
gaatgggtaa	gccctctcca	ttgtgttcct	aaaaaggag	gtattaccgt	tgttcttaat	120
gataaagatg	aattgatccc	gcaaataatt	attacagggt	ataggatggt	aattgatttc	180
cataagttaa	ataaagctac	taagaaagat	cattaccctt	tacctcttat	tgatcaaatt	240
ctagaaagac	tatccaaaca	cacacatttc	tgctttctag	atggttatac	tggtttctct	300
caaataacctg	tgtcagtgaa	ggatcaatct	aaaactactt	ttacttgccc	ttttggtact	360
tttgcttata	gacttatgcc	ttttggttta	tgtaatgcac	ctacttcctt	tcaaagatgc	420
atgatggcta	tattctctgt	tttttggtgaa	aatatttggt	aggtattcat	ggatgatttc	480
tccggttatg	gacccctctt	tgatgattgt	ttgagcaacc	ttgatcgagt	tttgagaga	540
tgcaagaca	ctagtctcat	cctgaattgg	gaaaagtgtc	actttatggt	taatgaaggc	600
attgtcttgg	ggcataagat	ttccgagaga	ggtattgaag	ttgacaaagc	caaagttgat	660
gctattgaaa	agattccatg	tccaaggac	ataaaaggta	taagaagttt	ccttggtcat	720
gctgggtttt	ataggagggt	catcaaagac	ttctcaaagg	tt		762

<210> 89

<211> 254

<212> PRT

<213> Triticum aestivum

<400> 89

Val Arg Lys Glu Val Phe Lys Phe Leu Glu Ala Gly Ile Thr Tyr Pro
 1 5 10 15
 Val Ala Asp Ser Glu Trp Val Ser Pro Leu His Cys Val Pro Lys Lys
 20 25 30
 Gly Gly Ile Thr Val Val Leu Asn Asp Lys Asp Glu Leu Ile Pro Gln
 35 40 45
 Ile Ile Ile Thr Gly Tyr Arg Met Val Ile Asp Phe His Lys Leu Asn
 50 55 60
 Lys Ala Thr Lys Lys Asp His Tyr Pro Leu Pro Leu Ile Asp Gln Ile
 65 70 75 80
 Leu Glu Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asp Gly Tyr
 85 90 95
 Thr Gly Phe Ser Gln Ile Pro Val Ser Val Lys Asp Gln Ser Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Leu Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Thr Ser Phe Gln Arg Cys Met Met Ala Ile
 130 135 140
 Phe Ser Val Phe Cys Glu Asn Ile Cys Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg
 165 170 175
 Val Leu Gln Arg Cys Glu Asp Thr Ser Leu Ile Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser
 195 200 205
 Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Ile Glu Lys
 210 215 220
 Ile Pro Cys Pro Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Ser Lys Val
 245 250

<210> 90

<211> 791

<212> DNA

<213> Gossypium hirsutum

<400> 90

gtgcgcaagg aggttttaaa gctacttgat gacgggatga tctatcccat atctaacagt 60
 aattgggtta gccagtagca catagtagca aaaaagacca gtgcaaccgt aatcgagaat 120
 tcggcagggt agatagttcc cactcgggtc caaaacgggt ggagagtatg catcgattac 180
 aggaagtga attccttaac tcggaaggat cactttccac ttccttttat tgaccagatg 240
 ttagaacgtt tagctggaaa gtctcattat ttagaacgtt tagctggaaa gtctcattat 300
 tgttgtttgg atggttacta aggttttttc cagatcccag tggcaccgga ggatcaagaa 360
 agacaatgtt tacgtgcca tttggcacgt tttcttacag acggatgccg ttcggactct 420
 gtaatgcacc agccagtttt cataggtgca tggttaagtat attttcagac tacgtcgata 480
 aaattatcga ggtgttcatt gacgacttta ctgtatatgg tgagtccttc gaggtaagtc 540
 tgacgaacct tgcaaaaatt ttggaaagat gcttagaatt taatcttggt ctaaattatg 600
 agaaatgccca ttttatggta gacaagggt tagttctagg tcatattatt tctgctgatg 660
 gaatttctgt tgataaagca aaaatcaaca tcattaactc actaccatac cccacaactg 720
 tgagggagat ttggtctttc cttggtcatg caggtttcta caagtgggtc atcaaagact 780
 tttcaaaagt t 791

<210> 91
 <211> 264
 <212> PRT
 <213> Gossypium hirsutum

<400> 91
 Val Arg Lys Glu Val Leu Lys Leu Leu Asp Asp Gly Met Ile Tyr Pro
 1 5 10 15
 Ile Ser Asn Ser Asn Trp Val Ser Pro Val His Ile Val Pro Lys Lys
 20 25 30
 Thr Ser Ala Thr Val Ile Glu Asn Ser Ala Gly Glu Ile Val Pro Thr
 35 40 45
 Arg Val Gln Asn Gly Trp Arg Val Cys Ile Asp Tyr Arg Lys Leu Asn
 50 55 60
 Ser Leu Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Ala Gly Lys Ser His Tyr Leu Glu Arg Leu Ala Gly
 85 90 95
 Lys Ser His Tyr Cys Cys Leu Asp Gly Tyr Glx Gly Phe Phe Gln Ile
 100 105 110
 Pro Val Ala Pro Glu Asp Gln Glu Lys Thr Met Phe Thr Cys Pro Phe
 115 120 125
 Gly Thr Phe Ser Tyr Arg Arg Met Pro Phe Gly Leu Cys Asn Ala Pro
 130 135 140
 Ala Ser Phe His Arg Cys Met Val Ser Ile Phe Ser Asp Tyr Val Asp
 145 150 155 160
 Lys Ile Ile Glu Val Phe Met Asp Asp Phe Thr Val Tyr Gly Glu Ser
 165 170 175
 Phe Glu Val Ser Leu Thr Asn Leu Ala Lys Ile Leu Glu Arg Cys Leu
 180 185 190
 Glu Phe Asn Leu Val Leu Asn Tyr Glu Lys Cys His Phe Met Val Asp
 195 200 205
 Lys Gly Leu Val Leu Gly His Ile Ile Ser Ala Asp Gly Ile Ser Val
 210 215 220
 Asp Lys Ala Lys Ile Asn Ile Ile Asn Ser Leu Pro Tyr Pro Thr Thr
 225 230 235 240
 Val Arg Glu Ile Trp Ser Phe Leu Gly His Ala Gly Phe Tyr Lys Trp
 245 250 255
 Phe Ile Lys Asp Phe Ser Lys Val
 260

<210> 92
 <211> 763
 <212> DNA
 <213> Gossypium hirsutum

<400> 92
 gtgcgtaaag aggtcgtaaa gctacttgat tccgggatga tctatcccat atctgacaat 60
 aattgggtta gtccagtcca catagtaccc aaaaagaccg gtgtaaccgt aattgagaat 120
 tcagcaggtg agatgggttcc cacttaagtc cgaaacggtc ggagagtatg catcgattac 180
 aggaagttga attccttaac tcggaaagat cactttccac ttctttttat tgatcagatg 240
 ttagaacatt tagccagaaa gtctcattat tgttgtctgg atggttactc aggttttttc 300
 cagatcccaa tggcactaaa ggatcaagaa aagatgacat ttacgtgcc atttggcatg 360
 ttcgcttata gaaggatgtc gtttcagact ttgcaatgca ccaaccatgt ttcagaggtg 420
 catgataagt atattttttg actatgttaa gaaaataatt gaggtgttca tggacgaatt 480
 tactgtatat agtgagtcct tcgaggtata tttgtcaaat ctagaaaaat ttttgaaaag 540
 atgcttagaa tttaatcttg ttctaaatta tgagaattgc tatttaatgg tagacaaggg 600

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attagttcta ggtcatatca tttctgctaa gggaatttct gtcgataaag taaaaattaa 660
catcataagc tcaataccat accccacaac tgtgaggag attcgttctt tccttagtca 720
tataggtttc tataggcgat tcatcaagga cttttcaaaa gtt 763

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<210> 93

<211> 254

<212> PRT

<213> *Gossypium hirsutum*

<400> 93

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Val Arg Lys Glu Val Val Lys Leu Leu Asp Ser Gly Met Ile Tyr Pro
 1           5           10           15
Ile Ser Asp Asn Asn Trp Val Ser Pro Val His Ile Val Pro Lys Lys
          20           25           30
Thr Gly Val Thr Val Ile Glu Asn Ser Ala Gly Glu Met Val Pro Thr
          35           40           45
Glx Val Arg Asn Gly Arg Arg Val Cys Ile Asp Tyr Arg Lys Leu Asn
          50           55           60
Ser Leu Thr Arg Lys Asp His Phe Pro Leu Leu Phe Ile Asp Gln Met
65           70           75           80
Leu Glu His Leu Ala Arg Lys Ser His Tyr Cys Cys Leu Asp Gly Tyr
          85           90           95
Ser Gly Phe Phe Gln Ile Pro Met Ala Leu Lys Asp Gln Glu Lys Met
          100          105          110
Thr Phe Thr Cys Pro Phe Gly Met Phe Ala Tyr Arg Arg Met Ser Phe
          115          120          125
Arg Leu Cys Asn Ala Pro Thr Met Phe Gln Arg Cys Met Ile Ser Ile
          130          135          140
Phe Phe Asp Tyr Val Lys Lys Ile Ile Glu Val Phe Met Asp Glu Phe
145          150          155          160
Thr Val Tyr Ser Glu Ser Phe Glu Val Tyr Leu Ser Asn Leu Glu Lys
          165          170          175
Phe Leu Glu Arg Cys Leu Glu Phe Asn Leu Val Leu Asn Tyr Glu Asn
          180          185          190
Cys Tyr Leu Met Val Asp Lys Gly Leu Val Leu Gly His Ile Ile Ser
          195          200          205
Ala Lys Gly Ile Ser Val Asp Lys Val Lys Ile Asn Ile Ile Ser Ser
          210          215          220
Ile Pro Tyr Pro Thr Thr Val Arg Glu Ile Arg Ser Phe Leu Ser His
225          230          235          240
Ile Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Ser Lys Val
          245          250

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<210> 94

<211> 723

<212> DNA

<213> *Gossypium hirsutum*

<400> 94

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gtgcgtaagg aggtttttgaa attgttggat gctggaatga tataactcgat ctttgacagt 60
gattgggtta gctgggttca tgtcgtgcc aagaaaactg gcgtgacagt ggtgaaaaac 120
tcatcaggag agctagtccc tacccgagtc cagaatcgat ggagggtttg catcgattac 180
aggaagtga acgcagctac ccgaaatgac cattttccac ttcccttcac tgatcaaatg 240
ctcgagcgat tagctaataa gaccattat tgttgtctcg atgggtactc aggacttttc 300
caaattccgg tggcacctga ggatcaagac aaaacaactt tcacgtgccc ctttggaacg 360
tttgcgata gaagaatgtc gtttgactc tgtaatgtc cggccactt ccagagatgt 420
atggtgagca tattctctga ttatgtcgag aaaatcattg aattcttcac ggatgacttc 480

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acgggtgtacg gtaactcttt taacgaatgt ctcgataatc ttgctaagat attacagaga      540
tgcctagaat ttaatcttgt tttaaattat gaaaaatgcc acttcatggg tgacaaagga      600
ttaattttgg gtcatatagt ttcttcagaa ggtattgagg tcaataaagc aaaaacgaat      660
attattgact cattacctta ccccagattt tacagacgat tcataaagga cttcacaaaa      720
gtt                                                                    723

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<210> 95

<211> 241

<212> PRT

<213> *Gossypium hirsutum*

<400> 95

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Val Arg Lys Glu Val Leu Lys Leu Leu Asp Ala Gly Met Ile Tyr Ser
 1           5           10          15
Ile Phe Asp Ser Asp Trp Val Ser Trp Val His Val Val Pro Lys Lys
          20          25          30
Thr Gly Val Thr Val Val Lys Asn Ser Ser Gly Glu Leu Val Pro Thr
          35          40          45
Arg Val Gln Asn Arg Trp Arg Val Cys Ile Asp Tyr Arg Lys Leu Asn
          50          55          60
Ala Ala Thr Arg Asn Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met
65          70          75          80
Leu Glu Arg Leu Ala Asn Lys Thr His Tyr Cys Cys Leu Asp Gly Tyr
          85          90          95
Ser Gly Leu Phe Gln Ile Pro Val Ala Pro Glu Asp Gln Asp Lys Thr
          100         105         110
Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Ser Phe
          115         120         125
Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Val Ser Ile
          130         135         140
Phe Ser Asp Tyr Val Glu Lys Ile Ile Glu Phe Phe Met Asp Asp Phe
145         150         155         160
Thr Val Tyr Gly Asn Ser Phe Asn Glu Cys Leu Asp Asn Leu Ala Lys
          165         170         175
Ile Leu Gln Arg Cys Leu Glu Phe Asn Leu Val Leu Asn Tyr Glu Lys
          180         185         190
Cys His Phe Met Val Asp Lys Gly Leu Ile Leu Gly His Ile Val Ser
          195         200         205
Ser Glu Gly Ile Glu Val Asn Lys Ala Lys Thr Asn Ile Ile Asp Ser
          210         215         220
Leu Pro Tyr Pro Arg Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys
225         230         235         240
Val

```

<210> 96

<211> 762

<212> DNA

<213> *Lycopersicon esculentum*

<400> 96

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gtgcgggaaag aggttgtgaa gctgttagat acgggtattg tctagccaat ttcggacaac      60
aagtaggtta gtccagtaca atgtgaacct aaaaaggagg acataacggg gatcactaat      120
gaaaaaaaaatg agttgatccc aaccatgata gtcacataat ggagaatatg catggattac      180
aggaaattga atgaagccac caggaaggac cattaccggg tcccttttat tgatcagatg      240
ttggaccggg ttgctgggga ataataattat tgttttctta atggctattt acggtacaac      300
caaatgtga tttcaccaaaa ggattaagag aaaaccactt tcacttgccc gtatggtaca      360

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tatgctttca aaaagatacc ttttgggtta tgaaatgcct cggctacttt ccaatgatgc 420
atgatggcta tttttcatga tatggttgaa gattttgttg agatattcat gaatgatttc 480
tcagtgtttg gggattcttt tgatatgtgc ttggagaatt tggacagtgt gttggctagt 540
tgtgaagaaa ctaatctttt cctaaactgg gaataatagc aatttctagt aaaggaaggg 600
attatgctag gacataaggt gtcaaagaga ggtatggaag ttgatagtgc caaagtggag 660
gttattgaaa agcttcccc tcctatatct gttaaaggga tgcaaagttt tctgggtcat 720
gttgggttct ataggagatt cataaaagac ttcacaaagg tt 762

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<210> 97

<211> 254

<212> PRT

<213> Lycopersicon esculentum

<400> 97

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Val Arg Lys Glu Val Val Lys Leu Leu Asp Thr Gly Ile Val Glx Pro
 1          5          10          15
Ile Ser Asp Asn Lys Glx Val Ser Pro Val Gln Cys Glu Pro Lys Lys
          20          25          30
Gly Asp Ile Thr Val Ile Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr
          35          40          45
Met Ile Val Thr Glx Trp Arg Ile Cys Met Asp Tyr Arg Lys Leu Asn
          50          55          60
Glu Ala Thr Arg Lys Asp His Tyr Pro Val Pro Phe Ile Asp Gln Met
65          70          75          80
Leu Asp Arg Leu Ala Gly Glu Glx Tyr Tyr Cys Phe Leu Asn Gly Tyr
          85          90          95
Leu Arg Tyr Asn Gln Ile Val Ile Ser Pro Lys Asp Glx Glu Lys Thr
          100          105          110
Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Phe Lys Lys Ile Pro Phe
          115          120          125
Gly Leu Glx Asn Ala Ser Ala Thr Phe Gln Glx Cys Met Met Ala Ile
          130          135          140
Phe His Asp Met Val Glu Asp Phe Val Glu Ile Phe Met Asn Asp Phe
145          150          155          160
Ser Val Phe Gly Asp Ser Phe Asp Met Cys Leu Glu Asn Leu Asp Ser
          165          170          175
Val Leu Ala Ser Cys Glu Glu Thr Asn Leu Phe Leu Asn Trp Glu Glx
          180          185          190
Glx Gln Phe Leu Val Lys Glu Gly Ile Met Leu Gly His Lys Val Ser
          195          200          205
Lys Arg Gly Met Glu Val Asp Ser Ala Lys Val Glu Val Ile Glu Lys
          210          215          220
Leu Pro Pro Pro Ile Ser Val Lys Gly Met Gln Ser Phe Leu Gly His
225          230          235          240
Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
          245          250

```

<210> 98

<211> 689

<212> DNA

<213> Lycopersicon esculentum

<400> 98

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cgaaaggagg tggtgaaact ggaaattatc aagtagttgg atgctagagt aatctatcca 60
atcgccgata gtagttgggt atgcctagtt cagtgtgtac caaagaaagg gggaatgact 120
gtggtcccca acgaaaagaa tgaacttggt cgaatgagac cggttactgg atggagggtg 180
tgcattggatt accgtaaact gaactcatag actgaaaaag actattttca tatgcccttc 240

```

```

atggatcaga tgttggatag acttgccgga aaaggggtggt attgttttct tgatgggtat 300
tcgggggtata atcagatttc tattgcacca gaagatcaag agaaaaccac tttcacttgt 360
ccatacggga cttttgcatt cagaagaatg tcgtttgggt tgtgcaatgc acccgcaacc 420
tttcagagat ggatgatgtc aatattttct gacatgatgg aggatactat agaggttttt 480
atggatgatt tttctgtggt tgggtgattca ttcgagcggg gcttgtccaa tttatctgag 540
gttcttaaga gatgtgaaga ctgcaatttg gtactaaact gggaaaagtg tcatttcatg 600
gtgaaagagg gtattgtgtt gggtcacgcg atttcagaaa agggcatgca tgtttttact 660
ggtgattcat caaagacttc acaaagggtt 689

```

<210> 99

<211> 229

<212> PRT

<213> Lycopersicon esculentum

<400> 99

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Arg Lys Glu Val Val Lys Leu Glu Ile Ile Lys Glx Leu Asp Ala Arg
 1           5           10           15
Val Ile Tyr Pro Ile Ala Asp Ser Ser Trp Val Cys Leu Val Gln Cys
 20           25           30
Val Pro Lys Lys Gly Gly Met Thr Val Val Pro Asn Glu Lys Asn Glu
 35           40           45
Leu Val Arg Met Arg Pro Val Thr Gly Trp Arg Val Cys Met Asp Tyr
 50           55           60
Arg Lys Leu Asn Ser Glx Thr Glu Lys Asp Tyr Phe His Met Pro Phe
 65           70           75           80
Met Asp Gln Met Leu Asp Arg Leu Ala Gly Lys Gly Trp Tyr Cys Phe
 85           90           95
Leu Asp Gly Tyr Ser Gly Tyr Asn Gln Ile Ser Ile Ala Pro Glu Asp
 100          105          110
Gln Glu Lys Thr Thr Phe Thr Cys Pro Tyr Gly Thr Phe Ala Phe Arg
 115          120          125
Arg Met Ser Phe Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Trp
 130          135          140
Met Met Ser Ile Phe Ser Asp Met Met Glu Asp Thr Ile Glu Val Phe
 145          150          155          160
Met Asp Asp Phe Ser Val Val Gly Asp Ser Phe Glu Arg Cys Leu Ser
 165          170          175
Asn Leu Ser Glu Val Leu Lys Arg Cys Glu Asp Cys Asn Leu Val Leu
 180          185          190
Asn Trp Glu Lys Cys His Phe Met Val Lys Glu Gly Ile Val Leu Gly
 195          200          205
His Arg Ile Ser Glu Lys Gly Met His Val Phe Thr Gly Asp Ser Ser
 210          215          220
Lys Thr Ser Gln Arg
225

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<210> 100

<211> 760

<212> DNA

<213> Lycopersicon esculentum

<400> 100

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gtgcgtaagg aggtgtttta gcttctagat gcgggtattg tctacccaat taggacaaca 60
agtgggttag tctagtacaa tgtgtaccta aaaagggagg catggcaatg attactaatg 120
aaaacaatga gtttatccca accagcacag tcacaagatg gcgaatatgc atgaattaca 180
cgaagttaat gaagccacta ggaagaatca ttacccaatt ctttttattg attatatgtt 240
ggaccgggta gctgggcaag aatattattg ttttttggat tactaatcag ggtacaacta 300

```

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aatttttgatt gcaccagagg atcaagagaa aacaactttc acttgcccgt atggtacata 360
tgctttcaag aggatacctt ttgggttatg caatgctctg tctaatttcc aaagatgcat 420
gatgactatt tttcatgata tggttgaata ttttgaggat atattcatgg atgatttctt 480
agtgttttgg gagtcttttg atagatgctt ggagaatttg aacagggttg tagctagggtg 540
cgaacaaact aatcttgtcc tgaactggga aaaatgtcat ttttagtaa aggaagggaa 600
tttttcgggg cataaggtgt aaaagatagg gctggaagtt gatcatgaca aagtggaagt 660
aattgaaaag atctcctctc ccatttttgt gaaacgggtg agaagtttac taggtcatgc 720
tgagttttac aggatattca tcaaggactt ctcaaaggtt 760

```

<210> 101

<211> 254

<212> PRT

<213> *Lycopersicon esculentum*

<400> 101

```

Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Ile Val Tyr Pro
 1           5           10           15
Ile Ser Asp Asn Lys Trp Val Ser Leu Val Gln Cys Val Pro Lys Lys
          20           25           30
Gly Gly Met Ala Met Ile Thr Asn Glu Asn Asn Glu Phe Ile Pro Thr
          35           40           45
Ser Thr Val Thr Arg Trp Arg Ile Cys Met Asn Tyr Thr Lys Leu Asn
          50           55           60
Glu Ala Thr Arg Lys Asn His Tyr Pro Ile Leu Phe Ile Asp Tyr Met
          65           70           75           80
Leu Asp Arg Leu Ala Gly Gln Glu Tyr Tyr Cys Phe Leu Asp Tyr Glx
          85           90           95
Ser Gly Tyr Asn Glx Ile Leu Ile Ala Pro Glu Asp Gln Glu Lys Thr
          100          105          110
Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Phe Lys Arg Ile Pro Phe
          115          120          125
Gly Leu Cys Asn Ala Leu Ser Asn Phe Gln Arg Cys Met Met Thr Ile
          130          135          140
Phe His Asp Met Val Glu Tyr Phe Glu Asp Ile Phe Met Asp Asp Phe
          145          150          155          160
Leu Val Phe Trp Glu Ser Phe Asp Arg Cys Leu Glu Asn Leu Asn Arg
          165          170          175
Leu Leu Ala Arg Cys Glu Gln Thr Asn Leu Val Leu Asn Trp Glu Lys
          180          185          190
Cys His Phe Leu Val Lys Glu Gly Asn Phe Ser Gly His Lys Val Glx
          195          200          205
Lys Ile Gly Leu Glu Val Asp His Asp Lys Val Glu Val Ile Glu Lys
          210          215          220
Ile Ser Ser Pro Ile Phe Val Lys Arg Val Arg Ser Leu Leu Gly His
          225          230          235          240
Ala Glu Phe Tyr Arg Ile Phe Ile Lys Asp Phe Ser Lys Val
          245          250

```

<210> 102

<211> 776

<212> DNA

<213> *Lycopersicon esculentum*

<400> 102

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gtgcggaaaag aagtgttttaa actggaatca ttaaattggtt ggatgctgga gtaatatatc 60
cgatctccga tagtagttgg gtatgcccta ttcagtgtgt acctaagaaa gggggaatga 120
ctgtggtccc caataagaaa aatgaacttg ttctaattgag accggttact ggagggtggg 180

```

```

tgtgtatgga ttaccgtaaa ttaaatgcat ggactgaaaa agaccatttt cctatgcctt 240
tcatggatca gatgttggat agacttgccg aaaaagggtg gtactgtttt cttgatggat 300
agtcagggta taattagatt tctattgcac cagaagatca agagaaaacc acatttactt 360
gtccatatgg gacctttgca ttgaagagaa tgtcgtttgg gttgtgcaat gcaccgcga 420
catttcacag atgtaaaaat gttgatattc ttcgacatgg tggatgatac tattgatgct 480
tttatggatg atttttctct tgttggtgaa tcattcgaga ggtgtttgaa ccatttatct 540
gatgtcctta agagatgtga agactgcaat ttagtactaa attgggaaaa atgccacttc 600
atggtgaaaa aagggtattgt tttgggtcat cgcattccag aaaagggtcat agaggttgat 660
cgagctaaag tagaggtaat agagagactt cccccactat ctctgtaaaa ggtgtgagaa 720
gctttcttgg gcatgcaagt ttttaccgga gattcatcaa agacttcaca aaagtt 776

```

<210> 103

<211> 258

<212> PRT

<213> *Lycopersicon esculentum*

<400> 103

```

Ala Glu Arg Ser Val Glx Thr Gly Ile Ile Lys Trp Leu Asp Ala Gly
  1           5           10           15
Val Ile Tyr Pro Ile Ser Asp Ser Ser Trp Val Cys Pro Ile Gln Cys
      20           25           30
Val Pro Lys Lys Gly Gly Met Thr Val Val Pro Asn Lys Lys Asn Glu
      35           40           45
Leu Val Leu Met Arg Pro Val Thr Gly Gly Trp Val Cys Met Asp Tyr
      50           55           60
Arg Lys Leu Asn Ala Trp Thr Glu Lys Asp His Phe Pro Met Pro Phe
      65           70           75           80
Met Asp Gln Met Leu Asp Arg Leu Ala Glu Lys Gly Trp Tyr Cys Phe
      85           90           95
Leu Asp Gly Glx Ser Gly Tyr Asn Glx Ile Ser Ile Ala Pro Glu Asp
      100          105          110
Gln Glu Lys Thr Thr Phe Thr Cys Pro Tyr Gly Thr Phe Ala Leu Lys
      115          120          125
Arg Met Ser Phe Gly Leu Cys Asn Ala Pro Ala Thr Phe His Arg Cys
      130          135          140
Lys Met Leu Ile Phe Phe Asp Met Val Asp Asp Thr Ile Asp Ala Phe
      145          150          155          160
Met Asp Asp Phe Ser Leu Val Gly Glu Ser Phe Glu Arg Cys Leu Asn
      165          170          175
His Leu Ser Asp Val Leu Lys Arg Cys Glu Asp Cys Asn Leu Val Leu
      180          185          190
Asn Trp Glu Lys Cys His Phe Met Val Lys Lys Gly Ile Val Leu Gly
      195          200          205
His Arg Ile Pro Glu Lys Gly Ile Glu Val Asp Arg Ala Lys Val Glu
      210          215          220
Val Ile Glu Arg Leu Pro Pro Pro Ile Ser Val Lys Gly Val Arg Ser
      225          230          235          240
Phe Leu Gly His Ala Ser Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr
      245          250          255
Lys Val

```

<210> 104

<211> 761

<212> DNA

<213> *Solanum tuberosum*

<400> 104

```

gtgcggaagg aggtacttaa attggttgat gcacggattg tgtacccaat atcagacagt    60
aaatgggtaa gtccagtaaa gtgtgtgccc aagaagggca gaatgacggt gttgactaat    120
gagaagaatg aggtaatccc cacaagaaca gtgactgggt gacggatttg catggactac    180
atgaagttga acgacgccac cagaaaggac cattatccgg tacctttcat tgataaaata    240
ttggataggt tggcaggaca tgagtactat tgttttcttg gtgtctactc aggggtacaat    300
cagattgtta ttgcaataga ggactagggtg aaaaccacct tcacctgttc gtatggcaca    360
tatgcgttca agcacatgcc attcggcttg tgcaatgccc tggccacatt tcagagatgc    420
atgttggcaa tcttccatga tatggtggag gattttgttg aagttttcat ggatgacttc    480
ttggtgtttg gtgagttctt tgaactttgt ttgactaatt ttgacagatt tcttgctagg    540
tgtgaagaga cgaatctggt gataaactga tagaagtgtc actttctggt tcgagagggg    600
attgtgttgg gacacaagat ctccaaaaat gggctgaaa. ttgacaaagc caacgtagag    660
gttattgaga aattgccacc cccatcacag tgaaggtaat taaaagctta ctaggacatg    720
cttggtttta tacgaggttc atcaaagact tcacaaagggt t                    761

```

<210> 105

<211> 254

<212> PRT

<213> Solanum tuberosum

<400> 105

```

Val Arg Lys Glu Val Leu Lys Leu Leu Asp Ala Arg Ile Val Tyr Pro
1      5      10      15
Ile Ser Asp Ser Lys Trp Val Ser Pro Val Lys Cys Val Pro Lys Lys
20     25     30
Gly Arg Met Thr Val Leu Thr Asn Glu Lys Asn Glu Val Ile Pro Thr
35     40     45
Arg Thr Val Thr Gly Glx Arg Ile Cys Met Asp Tyr Met Lys Leu Asn
50     55     60
Asp Ala Thr Arg Lys Asp His Tyr Pro Val Pro Phe Ile Asp Lys Ile
65     70     75     80
Leu Asp Arg Leu Ala Gly His Glu Tyr Tyr Cys Phe Leu Gly Val Tyr
85     90     95
Ser Gly Tyr Asn Gln Ile Val Ile Ala Ile Glu Asp Glx Val Lys Thr
100    105    110
Thr Phe Thr Cys Ser Tyr Gly Thr Tyr Ala Phe Lys His Met Pro Phe
115    120    125
Gly Leu Cys Asn Ala Leu Ala Thr Phe Gln Arg Cys Met Leu Ala Ile
130    135    140
Phe His Asp Met Val Glu Asp Phe Val Glu Val Phe Met Asp Asp Phe
145    150    155    160
Leu Val Phe Gly Glu Ser Phe Glu Leu Cys Leu Thr Asn Phe Asp Arg
165    170    175
Phe Leu Ala Arg Cys Glu Glu Thr Asn Leu Val Ile Asn Glx Glx Lys
180    185    190
Cys His Phe Leu Val Arg Glu Gly Ile Val Leu Gly His Lys Ile Ser
195    200    205
Lys Asn Gly Leu Lys Val Asp Lys Ala Asn Val Glu Val Ile Glu Lys
210    215    220
Leu Pro Pro Pro Ile Thr Val Lys Val Ile Lys Ser Leu Leu Gly His
225    230    235    240
Ala Trp Phe Tyr Thr Arg Phe Ile Lys Asp Phe Thr Lys Val
245    250

```

<210> 106

<211> 760

<212> DNA

<213> Solanum tuberosum

<400> 106

```

gtgcgtaaag aggttttcaa actgctagat gtcggtattg tatatccgat ttcagaaagc      60
aaatgggtca gcccagttta gtgtgtgcct aaaaaaagag gcatgccggt gatcaccaat      120
gaaaaaaatg agttgattcc aaccaggaca gtgacagggt ggcgaatatg catggattat      180
aggaaattga atgaggccac cagaaaggat cactgcccgg ttccttttat tgatcagatg      240
ctggacaggt tagttgggca agaataattat tgtttcctgg aaggctattc aggatacaac      300
caaattgtga ttgcaccaga ggaccaggag aaaactacat tcacttgtct gtatgggaca      360
tatgctttca agtgactgcc gtttgggcta tgcaatgctc cagccacctt ccaaagatga      420
atgatggcta tctttcatga tatggttgaa gattttgtgg agatattcat ggatgacttc      480
tcagtcttta gggagtcttt tgataggtgt ttggagaatt gggacagggt gctggctaga      540
tgcgaggaaa ctaatctcat cctaaactgg aaaaaatgtc atttcctagt aaatgaaggg      600
attgtattgg gccataaggt gtcaaagaga gggctggaag ttgatcgtgc caaagtggaa      660
gttattgaaa aactacctcc tccaatctgt taaaggggtg agaagctttc tgggtcatgc      720
tggtttttac aggagattta taaaggactt cacaaagggt      760

```

<210> 107

<211> 254

<212> PRT

<213> Solanum tuberosum

<400> 107

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Val Arg Lys Glu Val Phe Lys Leu Leu Asp Val Gly Ile Val Tyr Pro
 1           5           10           15
Ile Ser Glu Ser Lys Trp Val Ser Pro Val Glx Cys Val Pro Lys Lys
      20           25           30
Arg Gly Met Pro Val Ile Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr
      35           40           45
Arg Thr Val Thr Gly Trp Arg Ile Cys Met Asp Tyr Arg Lys Leu Asn
      50           55           60
Glu Ala Thr Arg Lys Asp His Cys Pro Val Pro Phe Ile Asp Gln Met
      65           70           75           80
Leu Asp Arg Leu Val Gly Gln Glu Tyr Tyr Cys Phe Leu Glu Gly Tyr
      85           90           95
Ser Gly Tyr Asn Gln Ile Val Ile Ala Pro Glu Asp Gln Glu Lys Thr
      100          105          110
Thr Phe Thr Cys Leu Tyr Gly Thr Tyr Ala Phe Lys Glx Leu Pro Phe
      115          120          125
Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Glx Met Met Ala Ile
      130          135          140
Phe His Asp Met Val Glu Asp Phe Val Glu Ile Phe Met Asp Asp Phe
      145          150          155          160
Ser Val Phe Arg Glu Ser Phe Asp Arg Cys Leu Glu Asn Trp Asp Arg
      165          170          175
Val Leu Ala Arg Cys Glu Glu Thr Asn Leu Ile Leu Asn Trp Lys Lys
      180          185          190
Cys His Phe Leu Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser
      195          200          205
Lys Arg Gly Leu Glu Val Asp Arg Ala Lys Val Glu Val Ile Glu Lys
      210          215          220
Leu Pro Pro Pro Ile Ser Val Lys Gly Val Arg Ser Phe Leu Gly His
      225          230          235          240
Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
      245          250

```

<210> 108

<211> 761
 <212> DNA
 <213> Solanum tuberosum

<400> 108
 gtgcgtaaag aggttttcaa gctctggatg caggtattgt ctatccaatt tcagacagca 60
 agtgggtcag tccagttcag tgtgtgccta aaaagggagg catgacgggtg atcactaatg 120
 aaaaaaatga gttgattcca accaggacag tgacaggatg gcgaatatgc atggattaca 180
 gaaaattaaa tgaagctacc agaaaggatc actaccgggt tcctttttatt gatcagatgc 240
 tggacagggt ggctggacaa gaatattatt gtttcttggga tggttattca ggatacaacc 300
 aaatagtgat tgcaccagag gaccagggga aaactacatt cacttgcttg tatgggacat 360
 atgtttccaa gagaatgtcg tttgggctat gcaatgctcc atccattttc caaagatgca 420
 tgatggccat cttccatgat aagggtgaag attttatgga aatattcatg gatgacttct 480
 cagtatttgg ggagtctttt gacagggtgct tggagaattt agacagagtg ttggctagat 540
 gcgaggaaac taattttgtc ctaaaactggg aaaaatgtca tttcctagtg aaggaaggga 600
 ttgtgttggg tcataagggtg tcaaagagag ggctggaagt tgatcgtgcc agagtggaaa 660
 taatcaaaaa gctacctccc ccaatttctg ttaaaggggt gcgaagtttt ttgggtcatg 720
 ttagtttcta cgaaagattc ataaaggact tcaccaagggt t 761

<210> 109
 <211> 254
 <212> PRT
 <213> Solanum tuberosum

<400> 109
 Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Ile Val Tyr Pro
 1 5 10 15
 Ile Ser Asp Ser Lys Trp Val Ser Pro Val Gln Cys Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Val Ile Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr
 35 40 45
 Arg Thr Val Thr Gly Trp Arg Ile Cys Met Asp Tyr Arg Lys Leu Asn
 50 55 60
 Glu Ala Thr Arg Lys Asp His Tyr Pro Val Pro Phe Ile Asp Gln Met
 65 70 75 80
 Leu Asp Arg Leu Ala Gly Gln Glu Tyr Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Tyr Asn Gln Ile Val Ile Ala Pro Glu Asp Gln Gly Lys Thr
 100 105 110
 Thr Phe Thr Cys Leu Tyr Gly Thr Tyr Val Ser Lys Arg Met Ser Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ser Ile Phe Gln Arg Cys Met Met Ala Ile
 130 135 140
 Phe His Asp Lys Val Glu Asp Phe Met Glu Ile Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Phe Gly Glu Ser Phe Asp Arg Cys Leu Glu Asn Leu Asp Arg
 165 170 175
 Val Leu Ala Arg Cys Glu Glu Thr Asn Phe Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Leu Val Lys Glu Gly Ile Val Leu Gly His Lys Val Ser
 195 200 205
 Lys Arg Gly Leu Glu Val Asp Arg Ala Arg Val Glu Ile Ile Lys Lys
 210 215 220
 Leu Pro Pro Pro Ile Ser Val Lys Gly Val Arg Ser Phe Leu Gly His
 225 230 235 240
 Val Ser Phe Tyr Glu Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 110
 <211> 762
 <212> DNA
 <213> Solanum tuberosum

<400> 110
 gtgcgtaagg aggtcctcaa gctgtctgat gcaggaattg tgtaccccat ttatgatata 60
 aagtggatca gcccagttca ctgtgtgccg aaaaagggag gcatgacgat tattactaat 120
 gaaaagaagg agttgatttc agctagaacg gtgatagagt ggcacatatg aatggactat 180
 aggagactaa atgaggcaac tagaaaaggaa cactaccag ttcctttcat tgatcaaatg 240
 ttggacaggt ttattgggca agagtattat tgtttcctag atggctattc aggatataat 300
 caaattgtga ttgcgccata agataaagag aaaactacat ttacttctct atatgggaca 360
 tatgccttca agagaatgtc gtttgggccg tgcaatgctc caaccacatt ccaaagatgc 420
 atgacagcca tttttcatga tatgggtcaaa tattttgtgg agatattcat ggatgaattc 480
 ttagtctttg gggagtcttt tgacacgtgt ctagaatatt tggacaatgt gcttgccaga 540
 tgtgagggaa ctaatcccgt cctcaactgg gaaaaatgtc attttctagt gaagaagggg 600
 attgtactag gccacaaggt ttcagaggaa ggactggaag ttgatcgtgg aaaagtagag 660
 gtaatttaaa agctaccccc tcaagtcttc gttaaagggg tgagaagggt ccttggtcat 720
 tctaggttcg aaatgagatt cataaaaagac ttcacaaaag tt 762

<210> 111
 <211> 254
 <212> PRT
 <213> Solanum tuberosum

<400> 111
 Val Arg Lys Glu Val Leu Lys Leu Ser Asp Ala Gly Ile Val Tyr Pro
 1 5 10 15
 Ile Tyr Asp Ile Lys Trp Ile Ser Pro Val His Cys Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Ile Ile Thr Asn Glu Lys Lys Glu Leu Ile Ser Ala
 35 40 45
 Arg Thr Val Ile Glu Trp His Ile Glx Met Asp Tyr Arg Arg Leu Asn
 50 55 60
 Glu Ala Thr Arg Lys Glu His Tyr Pro Val Pro Phe Ile Asp Gln Met
 65 70 75 80
 Leu Asp Arg Phe Ile Gly Gln Glu Tyr Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Tyr Asn Gln Ile Val Ile Ala Pro Glx Asp Lys Glu Lys Thr
 100 105 110
 Thr Phe Thr Ser Leu Tyr Gly Thr Tyr Ala Phe Lys Arg Met Ser Phe
 115 120 125
 Gly Pro Cys Asn Ala Pro Thr Thr Phe Gln Arg Cys Met Thr Ala Ile
 130 135 140
 Phe His Asp Met Val Lys Tyr Phe Val Glu Ile Phe Met Asp Glu Phe
 145 150 155 160
 Leu Val Phe Gly Glu Ser Phe Asp Thr Cys Leu Glu Tyr Leu Asp Asn
 165 170 175
 Val Leu Ala Arg Cys Glu Glu Thr Asn Pro Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Leu Val Lys Lys Gly Ile Val Leu Gly His Lys Val Ser
 195 200 205
 Glu Glu Gly Leu Glu Val Asp Arg Gly Lys Val Glu Val Ile Glx Lys
 210 215 220
 Leu Pro Pro Gln Val Phe Val Lys Gly Val Arg Arg Phe Leu Gly His
 225 230 235 240

Ser Arg Phe Glu Met Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 112
 <211> 762
 <212> DNA
 <213> Solanum tuberosum

<400> 112
 gtgcggaagg aggttttttaa gctgctggat gcgggtattg tataccagat ttcagatagc 60
 aaaggggtct acccgattta gtttgtgcct aaaaaatgca gcatgacagt gatcaccaat 120
 gaaaagaatg agctgattcc aaccaggaca gtgacagggt ggcgaaatag catggattat 180
 atgaagttga atgaggccac cagaaaggat cactacccga ttcattttat tgatcagatg 240
 ttggacaagt tagctgagta aaaatattat tgtttcttgg cttgttattc aagatacaac 300
 caatttctca ttgcaccaca ggaccaggag gaaactacat tcacttgtcc ttatgggaca 360
 tatgctttca agcgaatgtc gtttgggcta tgcaatgctc caaccacctt ccaaagatgc 420
 ataagggcta tctttcatga tatggttgaa gattttgtgg agatattcat ggatgacttc 480
 tcagtctttg ggtagtcttt tgagaggtgt ctggaaaatt ttgacagggt gctggctgta 540
 tgcgaggaaa ctaatttttt cctaaaactgg gaaaaatgtc attttctagt gaaggaaggg 600
 attgtattgg gacataaggt gtcaaaagtga aggcttgaag ttgatcgtgc caaagtggaa 660
 gtcgttgaaa acctaccttc cccattctct gttaaagggg tgagaagttt tttgggtcat 720
 gctggtttct ataggagatt tatcaaagac ttcactaagg tt 762

<210> 113
 <211> 254
 <212> PRT
 <213> Solanum tuberosum

<400> 113
 Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Ile Val Tyr Gln
 1 5 10 15
 Ile Ser Asp Ser Lys Gly Val Tyr Pro Ile Glx Phe Val Pro Lys Lys
 20 25 30
 Cys Ser Met Thr Val Ile Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr
 35 40 45
 Arg Thr Val Thr Gly Trp Arg Ile Cys Met Asp Tyr Met Lys Leu Asn
 50 55 60
 Glu Ala Thr Arg Lys Asp His Tyr Pro Ile His Phe Ile Asp Gln Met
 65 70 75 80
 Leu Asp Lys Leu Ala Glu Glx Lys Tyr Tyr Cys Phe Leu Ala Cys Tyr
 85 90 95
 Ser Arg Tyr Asn Gln Phe Leu Ile Ala Pro Gln Asp Gln Glu Thr
 100 105 110
 Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Phe Lys Arg Met Ser Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Thr Thr Phe Gln Arg Cys Ile Arg Ala Ile
 130 135 140
 Phe His Asp Met Val Glu Asp Phe Val Glu Ile Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Phe Gly Glx Ser Phe Glu Arg Cys Leu Glu Asn Phe Asp Arg
 165 170 175
 Val Leu Ala Val Cys Glu Glu Thr Asn Phe Phe Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Leu Val Lys Glu Gly Ile Val Leu Gly His Lys Val Ser
 195 200 205
 Lys Glx Arg Leu Glu Val Asp Arg Ala Lys Val Glu Val Val Glu Asn
 210 215 220

Leu Pro Ser Pro Phe Ser Val Lys Gly Val Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 114

<211> 793

<212> DNA

<213> Solanum tuberosum

<400> 114

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aacttttgtg aagtctttaa tgaaggatgt tgtcagagaa gaagtcatca agtggctgga      60
tacagggatt gtgtacccaa tatctgacaa taaatgggca agtccagtgc agtgtgtgcc      120
taaaaaggga ggaatgacag ttgtgaccaa tgagaaaaat gagttgatcc ccacaagaac      180
agtaactggg tggaggctat gcatggacta cagaaaactc aatgaagcca ccaggaagga      240
ccactattcg gtaccgttca ttgatcaaat gttagacagg ttggctggcc aagagtatta      300
ctgtttcctt gatggttatt caaggtataa ttagatcgtc attgcacctg aggatcaaga      360
gaatacgaca ttcacttgcc catatggcac gtatgcattc aaacgcttgc cattcggtt      420
gtgcaatgcc ccaaccctat ttcagagatg tatgatggca atcttccatg atatggtgga      480
agattttgtt aaagtataca tggacgattt ctcggtgttt ggtgagtcgt tcgaactttg      540
tttatcta at cgtgatagag ttcttactag gtgtgaggag accaatttgg tgctgaactg      600
ggagaagtgt cactttctgg tcagagaagg aattatgttg gggcagaaga tctccaaaag      660
tgggctagaa gtagacaagg cgaaggtgga agtgattgag aagttgccac caccaatata      720
agtaaaggga gtgcgaagct tccttggaca tgctggtttt tacaagaggt tcataaagga      780
cttttcaaag gtt

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<210> 115

<211> 264

<212> PRT

<213> Solanum tuberosum

<400> 115

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Thr Phe Val Lys Ser Leu Met Lys Asp Val Val Arg Glu Glu Val Ile
  1 5 10 15
Lys Trp Leu Asp Thr Gly Ile Val Tyr Pro Ile Ser Asp Asn Lys Trp
  20 25 30
Ala Ser Pro Val Gln Cys Val Pro Lys Lys Gly Gly Met Thr Val Val
  35 40 45
Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr Arg Thr Val Thr Gly Trp
  50 55 60
Arg Leu Cys Met Asp Tyr Arg Lys Leu Asn Glu Ala Thr Arg Lys Asp
  65 70 75 80
His Tyr Ser Val Pro Phe Ile Asp Gln Met Leu Asp Arg Leu Ala Gly
  85 90 95
Gln Glu Tyr Tyr Cys Phe Leu Asp Gly Tyr Ser Arg Tyr Asn Glx Ile
  100 105 110
Val Ile Ala Pro Glu Asp Gln Glu Asn Thr Thr Phe Thr Cys Pro Tyr
  115 120 125
Gly Thr Tyr Ala Phe Lys Arg Leu Pro Phe Gly Leu Cys Asn Ala Pro
  130 135 140
Thr Leu Phe Gln Arg Cys Met Met Ala Ile Phe His Asp Met Val Glu
  145 150 155 160
Asp Phe Val Lys Val Tyr Met Asp Asp Phe Ser Val Phe Gly Glu Ser
  165 170 175
Phe Glu Leu Cys Leu Ser Asn Arg Asp Arg Val Leu Thr Arg Cys Glu
  180 185 190
Glu Thr Asn Leu Val Leu Asn Trp Glu Lys Cys His Phe Leu Val Arg

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195					200					205					
Glu	Gly	Ile	Met	Leu	Gly	Gln	Lys	Ile	Ser	Lys	Ser	Gly	Leu	Glu	Val
210					215					220					
Asp	Lys	Ala	Lys	Val	Glu	Val	Ile	Glu	Lys	Leu	Pro	Pro	Pro	Ile	Glx
225					230					235					240
Val	Lys	Gly	Val	Arg	Ser	Phe	Leu	Gly	His	Ala	Gly	Phe	Tyr	Lys	Arg
245					250					255					
Phe	Ile	Lys	Asp	Phe	Ser	Lys	Val								
260															

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<210> 116
<211> 761
<212> DNA
<213> Platanus occidentalis
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<400>	116						
gtgcgtaagg	agggttttcaa	acttccttaa	gtttgagtga	tttatcctat	ttaggatagg		60
aattgggtca	gcccgggttca	agtggttcct	aaaaagattg	gaataaccgt	tgtgaaaaat		120
tagaatgatg	agttgggtcc	taccagtgtt	cagaatgggt	ggaggggtgt	atagattata		180
gaaaattgaa	tgttgtaacc	cgcaaggatc	acttcctttt	accttttatt	gatcaaatgc		240
ttgaaagggt	agttgggtcat	tcttactatt	gtttcctaga	tggttattca	agttatttcc		300
agattgtaat	tactccagag	gattaagaaa	agacaacttt	tacatgtcca	tttgggactt		360
ttgcatatcg	ttgcatgccc	tttggccttt	gcaatgcccc	aaccactttc	caaagggtga		420
tggtttagcat	attttcatat	tacattgaga	atatcataga	agtttttatg	gatgatttca		480
tagtttatag	agactccttt	aataattttt	tgcataacct	tacatttggt	cttcaaagat		540
gcatagaaac	taaccttgtg	ttaaattatg	aaaaatgtca	tttatgggtt	gaacaaggta		600
tagttttggg	tcatgttatt	tcatctaaag	gaattgaggt	agataaagct	aaagttgata		660
ttattcaatc	tttaccttat	ctcattagta	tgcggaaggt	tcatttcttt	cttggacatg		720
caggttttcta	ccgaagattc	attaaagact	ttacaaagggt	t			761

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<210> 117
<211> 254
<212> PRT
<213> Platanus occidentalis
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<400> 117															
Val	Arg	Lys	Glu	Val	Phe	Lys	Leu	Leu	Lys	Val	Glx	Val	Ile	Tyr	Pro
1				5					10					15	
Ile	Glx	Asp	Arg	Asn	Trp	Val	Ser	Pro	Val	Gln	Val	Val	Pro	Lys	Lys
			20					25					30		
Ile	Gly	Ile	Thr	Val	Val	Lys	Asn	Glx	Asn	Asp	Glu	Leu	Val	Pro	Thr
		35					40					45			
Ser	Val	Gln	Asn	Gly	Trp	Arg	Val	Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn
	50					55					60				
Val	Val	Thr	Arg	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met
65					70					75					80
Leu	Glu	Arg	Leu	Val	Gly	His	Ser	Tyr	Tyr	Cys	Phe	Leu	Asp	Gly	Tyr
				85					90					95	
Ser	Ser	Tyr	Phe	Gln	Ile	Val	Ile	Thr	Pro	Glu	Asp	Glx	Glu	Lys	Thr
			100					105					110		
Thr	Phe	Thr	Cys	Pro	Phe	Gly	Thr	Phe	Ala	Tyr	Arg	Cys	Met	Pro	Phe
		115					120					125			
Gly	Leu	Cys	Asn	Ala	Pro	Thr	Thr	Phe	Gln	Arg	Cys	Met	Val	Ser	Ile
	130					135					140				
Phe	Ser	Tyr	Tyr	Ile	Glu	Asn	Ile	Ile	Glu	Val	Phe	Met	Asp	Asp	Phe
145					150					155					160
Ile	Val	Tyr	Gly	Asp	Ser	Phe	Asn	Asn	Phe	Leu	His	Asn	Leu	Thr	Leu

Val	Leu	Gln	Arg	Cys	Ile	Glu	Thr	Asn	Leu	Val	Leu	Asn	Tyr	Glu	Lys
			180					185					190		
Cys	His	Phe	Met	Val	Glu	Gln	Gly	Ile	Val	Leu	Gly	His	Val	Ile	Ser
		195					200					205			
Ser	Lys	Gly	Ile	Glu	Val	Asp	Lys	Ala	Lys	Val	Asp	Ile	Ile	Gln	Ser
		210				215					220				
Leu	Pro	Tyr	Leu	Ile	Ser	Met	Arg	Lys	Val	His	Ser	Phe	Leu	Gly	His
					230					235					240
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
				245					250						

```
<210> 118
<211> 762
<212> DNA
<213> Platanus occidentalis
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<400>	118						
gtgcgtaagg	aagttttcaa	gcttcttgaa	gttgagtgga	tttatcttat	ttcgaatagc		60
aattggggtta	gccaggttca	agtggctcct	aaaaagactg	gaataaccgt	tgtgaaaaat		120
cagaatgatg	agttagttcc	tacctatggt	cagaatgggt	ggtggggttg	tataaattat		180
agaaaaattaa	atgttataac	ctgcaaggat	cacttccctt	taccttttat	tgataaaatg		240
cttgaaaggt	tagctggtca	ttcttactat	tgtttccttg	atggttattt	aggttatttt		300
caaattgcaa	ttacttcgga	ggatcaagaa	aagatgattt	ttaagtgcc	attcgggact		360
tttgcatatc	gtcacatgcc	ctttggcctt	tgcaatgcc	caaccacttt	ctaaaggtgt		420
atggttagca	tattttcaga	ttacattgag	aatatcatag	aagtctttat	ggatgatttc		480
acagtttatg	gagactcctt	tgataaattgt	ctgcataacc	ttacacttgt	tattcaaaga		540
tgcatagaaa	ctaaccctagt	gttaaattct	taaaaatgtc	attttatggt	tgaacaaggt		600
atagttttgg	gtcatgttgt	ttcatcttag	ggaattgagg	tagataaacc	taaaagtgat		660
attattcaaa	ctttacctta	ttcactagt	gtgcgagaag	ttcgttcttt	tcttggacat		720
gtaggttttt	actgaagatt	cataaaagac	ttcaciaaagg	tt			762

```
<210> 119
<211> 254
<212> PRT
<213> Platanus occidentalis
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<400> 119																
Val	Arg	Lys	Glu	Val	Phe	Lys	Leu	Leu	Glu	Val	Gly	Val	Ile	Tyr	Leu	
1				5					10					15		
Ile	Ser	Asn	Ser	Asn	Trp	Val	Ser	Pro	Val	Gln	Val	Ala	Pro	Lys	Lys	
			20					25					30			
Thr	Gly	Ile	Thr	Val	Val	Lys	Asn	Gln	Asn	Asp	Glu	Leu	Val	Pro	Thr	
		35					40					45				
His	Val	Gln	Asn	Gly	Trp	Trp	Val	Cys	Ile	Asn	Tyr	Arg	Lys	Leu	Asn	
	50					55					60					
Val	Ile	Thr	Cys	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Ile	Asp	Lys	Met	
65					70					75					80	
Leu	Glu	Arg	Leu	Ala	Gly	His	Ser	Tyr	Tyr	Cys	Phe	Leu	Asp	Gly	Tyr	
				85					90					95		
Leu	Gly	Tyr	Phe	Gln	Ile	Ala	Ile	Thr	Ser	Glu	Asp	Gln	Glu	Lys	Met	
			100					105					110			
Ile	Phe	Lys	Cys	Pro	Phe	Gly	Thr	Phe	Ala	Tyr	Arg	His	Met	Pro	Phe	
		115					120					125				
Gly	Leu	Cys	Asn	Ala	Pro	Thr	Thr	Phe	Glx	Arg	Cys	Met	Val	Ser	Ile	
	130					135					140					
Phe	Ser	Asp	Tyr	Ile	Glu	Asn	Ile	Ile	Glu	Val	Phe	Met	Asp	Asp	Phe	

```

145          150          155          160
Thr Val Tyr Gly Asp Ser Phe Asp Asn Cys Leu His Asn Leu Thr Leu
          165          170          175
Val Ile Gln Arg Cys Ile Glu Thr Asn Leu Val Leu Asn Ser Glx Lys
          180          185          190
Cys His Phe Met Val Glu Gln Gly Ile Val Leu Gly His Val Val Ser
          195          200          205
Ser Arg Gly Ile Glu Val Asp Lys Pro Lys Val Asp Ile Ile Gln Thr
          210          215          220
Leu Pro Tyr Ser Thr Ser Val Arg Glu Val Arg Ser Phe Leu Gly His
225          230          235          240
Val Gly Phe Tyr Glx Arg Phe Ile Lys Asp Phe Thr Lys Val
          245          250

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<210> 120

<211> 759

<212> DNA

<213> *Platanus occidentalis*

<400> 120

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gtgcggaaaag aggttttttaa gcttttggat gtagggatta tatacccaat tttttatagt      60
aattaggttaa gtcccactca agtggaccga agaattctgg tgtgactgta gttaaaaatg      120
caaatgatga attgattcca aatagactca ctattgggtg gcgtgatgc attaaactata      180
agaagttaa ctcagtgact aggaaggacc atttcccttt accattcatg actaaatcct      240
agaaagggtg gctggtcaca aattttatta tttcctatat gggtattcta gatataacta      300
aatagagatt gcacctgagg actaagaaaa taccactttt acatgtccat ttggcacttt      360
tgcttatcga aggatgtcat ttggattatg taatgctctt gccacgttct aaagatgcat      420
gttgagtata ttttagtgata tggtagaaca ttttcttgag gtgtttatgg attttttttg      480
tttttggtaa ttcatttgat gattgtttgc ataatttgaa aaaagtgtta aatagatgtg      540
aaggaaaaaa acatcatttt gaattgagag aagtgtcatt tcatggcttc taaaagaatt      600
gtacttggtc acattgtctc ctcccaagga attaaagtgg tcaaagccaa aattgaattg      660
atagtcaatt tgcctagccc aaagactctt aaagacattc gatcttttct aggtcatgca      720
ggatttaaca aaaggttcat caaagacttc acgaaagt      759

```

<210> 121

<211> 254

<212> PRT

<213> *Platanus occidentalis*

<400> 121

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Val Arg Lys Glu Val Phe Lys Leu Leu Asp Val Gly Ile Ile Tyr Pro
1          5          10          15
Ile Phe Tyr Ser Asn Glx Val Ser Pro Thr Gln Val Val Pro Lys Asn
          20          25          30
Ser Gly Val Thr Val Val Lys Asn Ala Asn Asp Glu Leu Ile Pro Asn
          35          40          45
Arg Leu Thr Ile Gly Trp Arg Val Cys Ile Asn Tyr Lys Lys Leu Asn
          50          55          60
Ser Val Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Glx Ile
65          70          75          80
Leu Glu Arg Val Ala Gly His Lys Phe Tyr Tyr Phe Leu Tyr Gly Tyr
          85          90          95
Ser Arg Tyr Asn Glx Ile Glu Ile Ala Pro Glu Asp Glx Glu Asn Thr
          100          105          110
Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Ser Phe
          115          120          125
Gly Leu Cys Asn Ala Leu Ala Thr Phe Glx Arg Cys Met Leu Ser Ile

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130	135	140
Phe Ser Asp Met Val Glu His Phe Leu Glu Val Phe Met Asp Asp Phe		
145	150	155
Phe Val Phe Gly Asn Ser Phe Asp Asp Cys Leu His Asn Leu Lys Lys		160
	165	170
Val Leu Asn Arg Cys Glu Glu Lys Asn Ile Ile Leu Asn Glx Glu Lys		175
	180	185
Cys His Phe Met Val Ser Lys Arg Ile Val Leu Gly His Ile Val Ser		190
	195	200
Ser Gln Gly Ile Lys Val Val Lys Ala Lys Ile Glu Leu Ile Val Asn		205
	210	215
Leu Pro Ser Pro Lys Thr Leu Lys Asp Ile Arg Ser Phe Leu Gly His		220
225	230	235
Ala Gly Phe Asn Lys Arg Phe Ile Lys Asp Phe Thr Lys Val		240
	245	250

<210> 122

<211> 761

<212> DNA

<213> *Platanus occidentalis*

<400> 122

tgcgtaaaga	ggtggtcaag	cttcttgaag	ttggagtgat	ttatcctatt	tcggatagca	60
attggggttag	cccggttcaa	gtgggtccta	aaaagactgg	aataaccggt	gtgaaaaatc	120
aaaatgatga	gtagttcct	accctgtgtc	agaatgggtg	gcaggtttgt	atagattata	180
taaaattaaa	tggtgtaacc	cgcaaggatc	acttcccttt	accttttatt	gatcaaagt	240
ttgaaagggt	agctgggtcat	tcttactatt	gtttccttga	tggatattca	tggtattttt	300
agattgcaat	tactccagag	gatcaagaaa	agacgacttt	tacgtgccca	ttcgggactt	360
tttcatatcg	ttgcatgccc	tttggccttt	gcaacgcccc	agccactttc	caaagggtga	420
tggttagcat	attttcagat	tacattgaga	atatcataga	agtctttatg	gatgatttca	480
tagtttatga	agactccttt	gataattgtc	tgcataacct	tacacttggt	ttttaaagat	540
gcatagaaac	taaccttggtg	ttaaattttg	aaaaatgtca	tgttatgggt	gaataaggta	600
tagttttggg	tcattgttgt	tcattctatg	gaattgaggt	agataaagtt	aaagttgata	660
ttattcaatc	tttaccttat	cccattagt	tcagggaagt	tcgttctttt	cttggacatg	720
cgggttttta	ccaaagattc	attaaagact	tcacgaaagt	t		761

<210> 123

<211> 253

<212> PRT

<213> *Platanus occidentalis*

<400> 123

Arg Lys Glu Val Val Lys Leu Leu Glu Val Gly Val Ile Tyr Pro Ile	
1	5
Ser Asp Ser Asn Trp Val Ser Pro Val Gln Val Val Pro Lys Lys Thr	
	20
Gly Ile Thr Val Val Lys Asn Gln Asn Asp Glu Leu Val Pro Thr Arg	
	35
Val Gln Asn Gly Trp Gln Val Cys Ile Asp Tyr Ile Lys Leu Asn Val	
	50
Val Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met Phe	
65	70
Glu Arg Leu Ala Gly His Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr Ser	
	85
Cys Tyr Phe Glx Ile Ala Ile Thr Pro Glu Asp Gln Glu Lys Thr Thr	
	100
Phe Thr Cys Pro Phe Gly Thr Phe Ser Tyr Arg Cys Met Pro Phe Gly	

115	120	125
Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Val Ser Ile Phe		
130	135	140
Ser Asp Tyr Ile Glu Asn Ile Ile Glu Val Phe Met Asp Asp Phe Ile		
145	150	155
Val Tyr Glu Asp Ser Phe Asp Asn Cys Leu His Asn Leu Thr Leu Val		
165	170	175
Phe Glx Arg Cys Ile Glu Thr Asn Leu Val Leu Asn Phe Glu Lys Cys		
180	185	190
His Val Met Val Glu Glx Gly Ile Val Leu Gly His Val Val Ser Ser		
195	200	205
Met Gly Ile Glu Val Asp Lys Val Lys Val Asp Ile Ile Gln Ser Leu		
210	215	220
Pro Tyr Pro Ile Ser Val Gln Glu Val Arg Ser Phe Leu Gly His Ala		
225	230	235
Gly Phe Tyr Gln Arg Phe Ile Lys Asp Phe Thr Lys Val		
245	250	

<210> 124

<211> 761

<212> DNA

<213> Sorghum bicolor

<400> 124

gtgcgtaaaag	aggtcttca	gctctatcat	gctgggatta	tttatcctgt	gccgcatagt	60
gagtgggtta	gccctgttca	agtagtgcca	aagaaaggag	gaatgacggt	cgtaggaat	120
gagaagaatg	aactcatccc	tcaacgaatt	gtcactgggt	ggcgtatgtg	tattgactat	180
caaaaaactca	acacggctac	aaagaaagat	aactttccgt	tacccttcat	tgatgaaatg	240
ttggaacggc	ttgcaaacca	ctctttcttc	tgtttccttg	atggttattc	tgatatacac	300
caaatcccaa	tccacccaga	tgaccaagaa	aagactacct	ttacatgccc	gtatggaact	360
tatgcataac	gacgaatgtc	gttcggactg	tgcaatgctc	cagcttcttt	ccaacgggtgc	420
atgatgtcta	ttttctcgga	catgattgag	aagatcatgg	aggttttcat	ggatgatttt	480
accgtctatg	gtaaaacctt	cgatcattgt	ttggagaatt	tagatagagt	cttgcagcga	540
tgtgaagaaa	agcacttaat	cctgaactgg	gagaaatgcc	attttatggg	tcaggaagga	600
atagtgctag	gacataaagt	gtccgaacgt	ggtatagagg	tggaacaaagc	aaagattgaa	660
gttattgaaa	aacttccacc	tcccacgaat	gtgaaaggat	ccgtagcttc	ttgggacatg	720
cagggttcta	tagatgcttc	ataaaaagact	tcacaaaggt	t		761

<210> 125

<211> 254

<212> PRT

<213> Sorghum bicolor

<400> 125

Val Arg Lys Glu Val Phe Lys Leu Tyr His Ala Gly Ile Ile Tyr Pro	
1 5 10 15	
Val Pro His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys	
20 25 30	
Gly Gly Met Thr Val Val Arg Asn Glu Lys Asn Glu Leu Ile Pro Gln	
35 40 45	
Arg Ile Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Gln Lys Leu Asn	
50 55 60	
Thr Ala Thr Lys Lys Asp Asn Phe Pro Leu Pro Phe Ile Asp Glu Met	
65 70 75 80	
Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr	
85 90 95	
Ser Gly Tyr His Gln Ile Pro Ile His Pro Asp Asp Gln Glu Lys Thr	

100	105	110
Thr Phe Thr Cys Pro Tyr Gly	Thr Tyr Ala Glx Arg Arg Met Ser Phe	
115	120	125
Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile		
130	135	140
Phe Ser Asp Met Ile Glu Lys Ile Met Glu Val Phe Met Asp Asp Phe		
145	150	155
Thr Val Tyr Gly Lys Thr Phe Asp His Cys Leu Glu Asn Leu Asp Arg		
165	170	175
Val Leu Gln Arg Cys Glu Glu Lys His Leu Ile Leu Asn Trp Glu Lys		
180	185	190
Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Val Ser		
195	200	205
Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Glu Val Ile Glu Lys		
210	215	220
Leu Pro Pro Pro Thr Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His		
225	230	235
Ala Gly Phe Tyr Arg Cys Phe Ile Lys Asp Phe Thr Lys Val		
245	250	

<210> 126
 <211> 762
 <212> DNA
 <213> Sorghum bicolor

<400> 126	
gtgcggaagg aggtccttaa attgctgcat gcagggatta tatatcctgt gccgcacagt	60
gagtgggtga gcccagtaca agttgtgcct aaaaaaggag gcatgactgt tattataaat	120
gaaaagaacg agctaattcc gcaacgcacc gtcacaggat ggcagatgtg catagactat	180
agaaaactaa acaaagccac gagaaaaggat cactttcctt taccttttat agatgagatg	240
ctagagcggg tagcaaacca ttcgttcttc tgtttcttag atggatattc agggatatcat	300
cagatcccga tccatcccga tgatcaaagc aaaaccactt ttacatgccc ttatggaact	360
tatgcttacc gtagaatgtc ttttggtgta tgtaaatgcac cagcttcttt tcaaagatgc	420
atgatgtcta tattttctga tatgattgaa gagattatgg aagttttcat ggatgatctc	480
tctgtttatg gaaaagcttt tgatagtgt cttgaaaact tagacaagg tttgcaaagt	540
tgtgaagaaa agcacttaat ccttaattgg gaaaaatgtc attttatgg tagggaagga	600
atagtgctag gacacttagt gtctgaaagg ggtattgagg tagacaaagc tgaaattgaa	660
gtaattgaac aactacctcc acctgtgaat ataaaaggaa ttcgaagctt tcttggccat	720
gctgggtttt atcgtagatt catcaaagat ttcacgaaag tt	762

<210> 127
 <211> 254
 <212> PRT
 <213> Sorghum bicolor

<400> 127	
Val Arg Lys Glu Val Leu Lys Leu Leu His Ala Gly Ile Ile Tyr Pro	
1 5 10 15	
Val Pro His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys	
20 25 30	
Gly Gly Met Thr Val Ile Ile Asn Glu Lys Asn Glu Leu Ile Pro Gln	
35 40 45	
Arg Thr Val Thr Gly Trp Gln Met Cys Ile Asp Tyr Arg Lys Leu Asn	
50 55 60	
Lys Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met	
65 70 75 80	
Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr	

				85						90					95				
Ser	Gly	Tyr	His	Gln	Ile	Pro	Ile	His	Pro	Asp	Asp	Gln	Ser	Lys	Thr				
			100					105				110							
Thr	Phe	Thr	Cys	Pro	Tyr	Gly	Thr	Tyr	Ala	Tyr	Arg	Arg	Met	Ser	Phe				
		115					120					125							
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Ser	Phe	Gln	Arg	Cys	Met	Met	Ser	Ile				
	130					135					140								
Phe	Ser	Asp	Met	Ile	Glu	Glu	Ile	Met	Glu	Val	Phe	Met	Asp	Asp	Phe				
145				150					155						160				
Ser	Val	Tyr	Gly	Lys	Ala	Phe	Asp	Ser	Cys	Leu	Glu	Asn	Leu	Asp	Lys				
			165					170				175							
Val	Leu	Gln	Ser	Cys	Glu	Glu	Lys	His	Leu	Ile	Leu	Asn	Trp	Glu	Lys				
		180						185				190							
Cys	His	Phe	Met	Val	Arg	Glu	Gly	Ile	Val	Leu	Gly	His	Leu	Val	Ser				
	195					200					205								
Glu	Arg	Gly	Ile	Glu	Val	Asp	Lys	Ala	Glu	Ile	Glu	Val	Ile	Glu	Gln				
	210					215					220								
Leu	Pro	Pro	Pro	Val	Asn	Ile	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His				
225				230						235					240				
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val						
			245					250											

<210> 128

<211> 762

<212> DNA

<213> Sorghum bicolor

<400> 128

gtgcggaagg	aagtcttaaa	gctttttacac	actaggatta	tttatctcgt	tcctcatagt	60
gagtgggtta	gcacggtaca	agttgtgcca	aagaaaggag	gaatgtcggg	tgtaggaat	120
gagaagaacg	aattcatccc	tcaacaaaact	gtcactgggt	ggcgtatgtg	cattgactac	180
caaaaactca	acaaggccac	aaggaaagat	cacttcccgt	tacctttcat	tgatgaaatg	240
ttgtaatggc	ttacaaatca	ctcgttcttt	tgtttccttg	aagggtattc	cagatatcat	300
caaatcccga	tccaccacga	tgaccaaaagt	aagactactt	tcacatgacc	ctatggaact	360
tacgcatacc	gacgaatgtc	gttcagggtta	tgtaatgctc	cagcttcttt	tcaacgggtgc	420
atgatgtcta	ttttttccaa	tatgattgag	aaaatcatgg	aggtattcac	ggatgatttt	480
accgtatatg	gcaaaacctt	tgatgattgt	ttagagaatt	tggaacaaagt	cttacaattg	540
tgtgaaggaa	agcacttaat	cgtaaaactag	gagaaatgcc	attttatggg	ccgagaagga	600
atagtgtctag	ggcacaagggt	gtccgaacgt	gggatatagg	tggaatagagc	caagattgaa	660
gttattgaaa	aacttccacc	tcccacaaat	gtgaaagaca	tccgcagttt	tcttggacat	720
gcagggttct	ataggcgctt	catcaaagat	ttcaccaagg	tt		762

<210> 129

<211> 254

<212> PRT

<213> Sorghum bicolor

<400> 129

Val	Arg	Lys	Glu	Val	Leu	Lys	Leu	Leu	His	Thr	Arg	Ile	Ile	Tyr	Leu
1				5					10					15	
Val	Pro	His	Ser	Glu	Trp	Val	Ser	Thr	Val	Gln	Val	Val	Pro	Lys	Lys
		20					25				30				
Gly	Gly	Met	Ser	Val	Val	Arg	Asn	Glu	Lys	Asn	Glu	Phe	Ile	Pro	Gln
	35					40				45					
Gln	Thr	Val	Thr	Gly	Trp	Arg	Met	Cys	Ile	Asp	Tyr	Gln	Lys	Leu	Asn
	50				55				60						
Lys	Ala	Thr	Arg	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Ile	Asp	Glu	Met

65		70		75		80									
Leu	Glx	Trp	Leu	Thr	Asn	His	Ser	Phe	Phe	Cys	Phe	Leu	Glu	Gly	Tyr
			85						90					95	
Ser	Arg	Tyr	His	Gln	Ile	Pro	Ile	His	His	Asp	Asp	Gln	Ser	Lys	Thr
			100					105					110		
Thr	Phe	Thr	Glx	Pro	Tyr	Gly	Thr	Tyr	Ala	Tyr	Arg	Arg	Met	Ser	Phe
		115					120					125			
Arg	Leu	Cys	Asn	Ala	Pro	Ala	Ser	Phe	Gln	Arg	Cys	Met	Met	Ser	Ile
	130					135					140				
Phe	Ser	Asn	Met	Ile	Glu	Lys	Ile	Met	Glu	Val	Phe	Thr	Asp	Asp	Phe
145					150				155					160	
Thr	Val	Tyr	Gly	Lys	Thr	Phe	Asp	Asp	Cys	Leu	Glu	Asn	Leu	Asp	Lys
			165					170					175		
Val	Leu	Gln	Leu	Cys	Glu	Gly	Lys	His	Leu	Ile	Val	Asn	Glx	Glu	Lys
		180						185				190			
Cys	His	Phe	Met	Val	Arg	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Val	Ser
	195						200				205				
Glu	Arg	Gly	Ile	Glu	Val	Asp	Arg	Ala	Lys	Ile	Glu	Val	Ile	Glu	Lys
	210					215					220				
Leu	Pro	Pro	Pro	Thr	Asn	Val	Lys	Asp	Ile	Arg	Ser	Phe	Leu	Gly	His
225					230				235					240	
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
			245					250							

<210> 130

<211> 761

<212> DNA

<213> Sorghum bicolor

<400> 130

gtgcgtaagg	agggtttttaa	gctgctgcat	gcagagatta	tatatcatgt	gccgcacagt	60
gagtgggtaa	gcccgattca	agttgtgcct	aaaaagggag	gcatgattgt	tgttacgaat	120
gaaaagaacg	agctaattcc	gcaacgcacc	gtcacagggt	ggcggatgtg	catagactat	180
agaaaactaa	acaaagccac	gagaaaggat	cattttcctt	tacctttcat	agatgagatg	240
ctagagcgat	tagcaaacca	ttcgttcttc	tgtttcttag	atggataatt	agggtatcac	300
cagatcccaa	tcaatcttga	tgatcaaagc	aaaaccactt	ttccatgccc	acatggaact	360
tatgcttacc	gtagaatgtc	ttttgggtta	tgtaatgcac	cagcttcttt	tcaaagatgc	420
atgatgtctg	tattttctaa	tatgattgaa	gagattatgg	aattttcatg	gatgatttct	480
ctgtttatgg	aaaaactttt	gatagtgtgc	ttgaaaactt	agacagggtt	ttgcaaagat	540
gtgaagaaaa	gtacttagtc	cttaattgga	aaaaatgtca	ttttatgggt	agggaaggaa	600
tagtgctggg	acacctagtg	tctgaaagag	gtattgaggt	cgacaaagct	aaaattgaag	660
taattgaaca	actacctcca	cctttgaata	taaaaggaat	tcgaagcttt	cttggccatg	720
ctgggttttta	tcgtagattc	attaaggact	ttacaaaggt	t		761

<210> 131

<211> 254

<212> PRT

<213> Sorghum bicolor

<400> 131

Val	Arg	Lys	Glu	Val	Phe	Lys	Leu	Leu	His	Ala	Glu	Ile	Ile	Tyr	His
1				5					10					15	
Val	Pro	His	Ser	Glu	Trp	Val	Ser	Pro	Val	Gln	Val	Val	Pro	Lys	Lys
		20					25					30			
Gly	Gly	Met	Ile	Val	Val	Thr	Asn	Glu	Lys	Asn	Glu	Leu	Ile	Pro	Gln
	35					40				45					
Arg	Thr	Val	Thr	Gly	Trp	Arg	Met	Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn

50		55		60
Lys Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met				
65		70		80
Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Glx				
	85		90	95
Leu Gly Tyr His Gln Ile Pro Ile Asn Leu Asp Asp Gln Ser Lys Thr				
	100		105	110
Thr Phe Pro Cys Pro His Gly Thr Tyr Ala Tyr Arg Arg Met Ser Phe				
	115		120	125
Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Val				
	130		135	140
Phe Ser Asn Met Ile Glu Glu Ile Met Glu Ile Phe Met Asp Asp Phe				
145		150		160
Ser Val Tyr Gly Lys Thr Phe Asp Ser Cys Leu Glu Asn Leu Asp Arg				
	165		170	175
Val Leu Gln Arg Cys Glu Glu Lys Tyr Leu Val Leu Asn Trp Lys Lys				
	180		185	190
Cys His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Leu Val Ser				
	195		200	205
Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Glu Val Ile Glu Gln				
	210		215	220
Leu Pro Pro Pro Leu Asn Ile Lys Gly Ile Arg Ser Phe Leu Gly His				
225		230		240
Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val				
	245		250	

<210> 132

<211> 763

<212> DNA

<213> Sorghum bicolor

<400> 132

gtgcggaag	aggtcgtcaa	gctctatcat	gctgggatta	tttatcctgt	gccacatagt	60
gagtgggta	gccctgttca	agtagtgcca	aagaaagaag	gaatgacggt	cgtaggaat	120
gagaagaatg	aactcatccc	tcaacaaatt	gtcactagat	ggcgtatgtg	tattgactat	180
cgaaaactca	acaaagctac	aaagaaagat	cactttccgt	tacccttcat	tgatgaaatg	240
ttggaatggc	ttgcaaacca	ctctttcttc	tgtttccttg	atggttattc	tgatatcac	300
caaatcccaa	tccaccaga	tgaccaagaa	aagactacct	ttacatgccc	gtattgaact	360
tatgcatact	gacgaatgtc	gttcggattg	tgcaatgtc	tagcttcttt	tccagcgggtg	420
catgatgtct	attttctcgg	acatgattga	gaagatcatg	gagggtttca	tggatgattt	480
taccgtctat	ggcaaaacct	tcgatcattg	tttgagaat	ttagatagag	tcttgacgag	540
atgtgaggaa	aatcacttaa	tcttgaactg	ggagaaatgt	cattttatgg	ttcaggaagg	600
aatagtgcta	ggacataaag	tgtccgaacg	tggtatagat	gtggacaaag	caaagattaa	660
agttattgaa	aaacttccac	ctcacacgaa	tgtgaaagga	atccatagct	ttttgggaca	720
tgcagggttc	tatagacgct	tcatcaagga	tttcacaaag	ggt		763

<210> 133

<211> 254

<212> PRT

<213> Sorghum bicolor

<400> 133

Val Arg Lys Glu Val Val Lys Leu Tyr His Ala Gly Ile Ile Tyr Pro						
1		5		10		15
Val Pro His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys						
	20		25		30	
Glu Gly Met Thr Val Val Arg Asn Glu Lys Asn Glu Leu Ile Pro Gln						

35	40	45
Gln Ile Val Thr Arg Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn		
50	55	60
Lys Ala Thr Lys Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met		
65	70	75
Leu Glu Trp Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr		
85	90	95
Ser Gly Tyr His Gln Ile Pro Ile His Pro Asp Asp Gln Glu Lys Thr		
100	105	110
Thr Phe Thr Cys Pro Tyr Glx Thr Tyr Ala Tyr Glx Arg Met Ser Phe		
115	120	125
Gly Leu Cys Asn Ala Leu Ala Ser Phe Gln Arg Cys Met Met Ser Ile		
130	135	140
Phe Ser Asp Met Ile Glu Lys Ile Met Glu Val Phe Met Asp Asp Phe		
145	150	155
Thr Val Tyr Gly Lys Thr Phe Asp His Cys Leu Glu Asn Leu Asp Arg		
165	170	175
Val Leu Gln Arg Cys Glu Glu Asn His Leu Ile Leu Asn Trp Glu Lys		
180	185	190
Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Val Ser		
195	200	205
Glu Arg Gly Ile Asp Val Asp Lys Ala Lys Ile Lys Val Ile Glu Lys		
210	215	220
Leu Pro Pro His Thr Asn Val Lys Gly Ile His Ser Phe Leu Gly His		
225	230	235
Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val		
245	250	

<210> 134

<211> 756

<212> DNA

<213> Sorghum bicolor

<400> 134

aaggaggttt	tcaagttgct	gcatgcaggg	attatatatc	ttgtgccgca	tagtgagtgg	60
gtaagcccag	ttcaagttgt	gcctaaaaag	ggaggcatga	ctattattat	gaatgaaaag	120
aacgagctaa	ttccgcaacg	caccgttaca	gtatggcgga	tgtgcataga	ctatagaaaa	180
ctaaacaaag	ccacgagaga	ggatcacttt	cctttacctt	tcatagatga	gatgctagag	240
tggttagcaa	accattcggt	cttctgtttc	ttagatggat	attgagggta	tcatcagatc	300
ccgatccatc	ccgatgatca	aagcaaaacc	acttttacat	gcccataatg	aacttatgct	360
taccgtagaa	tgtcttttgg	ggttatgta	gcactagctt	cttttcaaag	atgcatgatg	420
tctatatatt	ctgatatgat	tgaagagatt	atggaagttt	tcattggatga	tttctctgtt	480
tatggaaaaa	cttttgatag	ttgtcttaaa	aacttagaca	aggttttgca	aagatgtgaa	540
gaaaagcact	tagtccttaa	ttgggaaaaa	tgtcatttca	tggttaggga	aggaatagtg	600
ctgggacact	tagtgtctga	aagagctatt	gaggtagata	aagctaaaaa	tgaagtaatt	660
gaacaactac	gtccacctgt	gaacataaaa	ggaatttgaa	gctttcttgg	ccatgctggg	720
tttcatcgta	gattcataaa	agactttaca	aaggtt			756

<210> 135

<211> 252

<212> PRT

<213> Sorghum bicolor

<400> 135

Lys Glu Val Phe Lys Leu Leu His Ala Gly Ile Ile Tyr Leu Val Pro
1 5 10 15
His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys Gly Gly

Met	Thr	Ile	Ile	Met	Asn	Glu	Lys	Asn	Glu	Leu	Ile	Pro	Gln	Arg	Thr
	35						40					45			
Val	Thr	Val	Trp	Arg	Met	Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn	Lys	Ala
	50					55					60				
Thr	Arg	Glu	Asp	His	Phe	Pro	Leu	Pro	Phe	Ile	Asp	Glu	Met	Leu	Glu
65					70					75					80
Trp	Leu	Ala	Asn	His	Ser	Phe	Phe	Cys	Phe	Leu	Asp	Gly	Tyr	Glx	Gly
			85					90					95		
Tyr	His	Gln	Ile	Pro	Ile	His	Pro	Asp	Asp	Gln	Ser	Lys	Thr	Thr	Phe
			100					105					110		
Thr	Cys	Pro	Tyr	Gly	Thr	Tyr	Ala	Tyr	Arg	Arg	Met	Ser	Phe	Gly	Leu
	115						120					125			
Cys	Asn	Ala	Leu	Ala	Ser	Phe	Gln	Arg	Cys	Met	Met	Ser	Ile	Phe	Ser
	130					135					140				
Asp	Met	Ile	Glu	Glu	Ile	Met	Glu	Val	Phe	Met	Asp	Asp	Phe	Ser	Val
145					150					155					160
Tyr	Gly	Lys	Thr	Phe	Asp	Ser	Cys	Leu	Lys	Asn	Leu	Asp	Lys	Val	Leu
			165					170					175		
Gln	Arg	Cys	Glu	Glu	Lys	His	Leu	Val	Leu	Asn	Trp	Glu	Lys	Cys	His
		180					185						190		
Phe	Met	Val	Arg	Glu	Gly	Ile	Val	Leu	Gly	His	Leu	Val	Ser	Glu	Arg
	195						200					205			
Ala	Ile	Glu	Val	Asp	Lys	Ala	Lys	Ile	Glu	Val	Ile	Glu	Gln	Leu	Arg
	210					215					220				
Pro	Pro	Val	Asn	Ile	Lys	Gly	Ile	Glx	Ser	Phe	Leu	Gly	His	Ala	Gly
225					230					235					240
Phe	His	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val				
			245					250							

<210> 136
 <211> 762
 <212> DNA
 <213> Glycine max

<400> 136

gtgcgtaagg	aggttgtcaa	gcttttggag	gttgggctca	tatacctcat	ctctgacagc	60
gcttgggtaa	gcctagtaca	ggtggctccc	aagaaatgcg	gaatgacagt	ggtacaaaat	120
gagaggaatg	acttgatacc	aacacgaact	gtcactggct	agcggatgtg	tatcgactac	180
tgcaagttga	atgaagccac	acggaaggac	catttcccct	tacctttcat	ggatcagatg	240
ctggagaggc	ttgcagggca	ggcatactac	tgtttcttgg	atagatattc	aggatacaac	300
caaatcgcgg	tagaccccag	agatcaggag	aagatggcct	ttacatgccc	ctttggcgctc	360
tttgcttaca	gaaggatgtc	attcagggtta	tgtaacgcac	cagccacatt	tcagaggtgc	420
gtgctggcca	ttttttcaga	catggtggag	aagagcatcg	aggtatttat	ggatgaattc	480
tcgatttttg	gacccttatt	tgacagttgc	ttaaggaaact	tagagatggg	actacagagg	540
tcggtataga	ctaacttggt	actaaattag	gaaaaatgtc	atttcatggg	tcgagagggg	600
atagtgatgg	accacaatat	ctcagctaga	gggattgagg	ttgatcaggc	aaagatagac	660
gtcattgaga	agttgccacc	accactgaat	gttaaaggcg	tcagaagttt	cttagggcat	720
gcaggtttct	acaggaggtt	tatcaaggac	ttcaccaagg	tt		762

<210> 137
 <211> 254
 <212> PRT
 <213> Glycine max

<400> 137

Val	Arg	Lys	Glu	Val	Val	Lys	Leu	Leu	Glu	Val	Gly	Leu	Ile	Tyr	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1	5	10	15
Ile Ser Asp Ser Ala Trp Val Ser Leu Val Gln Val Ala Pro Lys Lys			
	20	25	30
Cys Gly Met Thr Val Val Gln Asn Glu Arg Asn Asp Leu Ile Pro Thr			
	35	40	45
Arg Thr Val Thr Gly Glx Arg Met Cys Ile Asp Tyr Cys Lys Leu Asn			
	50	55	60
Glu Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met			
65	70	75	80
Leu Glu Arg Leu Ala Gly Gln Ala Tyr Tyr Cys Phe Leu Asp Arg Tyr			
	85	90	95
Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Arg Asp Gln Glu Lys Met			
	100	105	110
Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Ser Phe			
	115	120	125
Arg Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Val Leu Ala Ile			
	130	135	140
Phe Ser Asp Met Val Glu Lys Ser Ile Glu Val Phe Met Asp Glu Phe			
145	150	155	160
Ser Ile Phe Gly Pro Leu Phe Asp Ser Cys Leu Arg Asn Leu Glu Met			
	165	170	175
Val Leu Gln Arg Cys Val Glx Thr Asn Leu Val Leu Asn Glx Glu Lys			
	180	185	190
Cys His Phe Met Val Arg Glu Gly Ile Val Met Asp His Asn Ile Ser			
	195	200	205
Ala Arg Gly Ile Glu Val Asp Gln Ala Lys Ile Asp Val Ile Glu Lys			
	210	215	220
Leu Pro Pro Pro Leu Asn Val Lys Gly Val Arg Ser Phe Leu Gly His			
225	230	235	240
Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val			
	245	250	

<210> 138
 <211> 763
 <212> DNA
 <213> Glycine max

<400> 138	
gtgcgtaagg aggtctttaa gttcttggag gctggggtca tatatcccat ctctaatagc	60
acttaggtaa gcccgagtaca ggtggttccc aagaaagggtg gaatgacagt agtacagaat	120
gagaagaatg acttgataacc aacacgaact gtcactagct ggccaatatg catcgattat	180
cgcaagctga atgaggccac ccggaaggac cacttccctc tacctttcat ggatcagatg	240
ttggagagac ttgcagggca ggcgtattat tgtttcttgg atggatactc gagatataat	300
cagattgcgg tggaccctag agaccaagag aagacgacct tcacatgccc tttttggcgt	360
ctttgcttac agaaggatgc cattcgggtt atgtaatgca ccagccacat ttcagagggtg	420
catgctggcc attttttcag acatggtgga gaaaaatatac gaggtattca tggatgactt	480
ttcagttttt gggccctcat ttgacagttg tttgaggaac ctagagatgg tacttttagag	540
gtgcgtagag actaattttag tgctgaactg ggagaagtgt catttttatgg ttcgagaggg	600
catagtcttg agccacaaga tctcagctag agggattgag gttgaccggg caaagataga	660
cgtcatagag aagctgccac caccattgaa tattaaagggt gtcagaagtt tcttagggca	720
tgcaggattc tacaggagat tcataaagga ctttacaaag gtt	763

<210> 139
 <211> 254
 <212> PRT
 <213> Glycine max

<400> 139

Val	Arg	Lys	Glu	Val	Phe	Lys	Phe	Leu	Glu	Ala	Gly	Leu	Ile	Tyr	Pro
1				5					10					15	
Ile	Ser	Asn	Ser	Thr	Glx	Val	Ser	Pro	Val	Gln	Val	Val	Pro	Lys	Lys
			20					25					30		
Gly	Gly	Met	Thr	Val	Val	Gln	Asn	Glu	Lys	Asn	Asp	Leu	Ile	Pro	Thr
		35					40					45			
Arg	Thr	Val	Thr	Ser	Trp	Arg	Ile	Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn
		50				55					60				
Glu	Ala	Thr	Arg	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Met	Asp	Gln	Met
65					70					75				80	
Leu	Glu	Arg	Leu	Ala	Gly	Gln	Ala	Tyr	Tyr	Cys	Phe	Leu	Asp	Gly	Tyr
				85				90						95	
Ser	Arg	Tyr	Asn	Gln	Ile	Ala	Val	Asp	Pro	Arg	Asp	Gln	Glu	Lys	Thr
			100					105					110		
Thr	Phe	Thr	Cys	Pro	Phe	Gly	Val	Phe	Ala	Tyr	Arg	Arg	Met	Pro	Phe
		115				120						125			
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Cys	Met	Leu	Ala	Ile
	130					135					140				
Phe	Ser	Asp	Met	Val	Glu	Lys	Asn	Ile	Glu	Val	Phe	Met	Asp	Asp	Phe
145					150					155				160	
Ser	Val	Phe	Gly	Pro	Ser	Phe	Asp	Ser	Cys	Leu	Arg	Asn	Leu	Glu	Met
			165					170						175	
Val	Leu	Glx	Arg	Cys	Val	Glu	Thr	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys
		180						185					190		
Cys	His	Phe	Met	Val	Arg	Glu	Gly	Ile	Val	Leu	Ser	His	Lys	Ile	Ser
		195					200					205			
Ala	Arg	Gly	Ile	Glu	Val	Asp	Arg	Ala	Lys	Ile	Asp	Val	Ile	Glu	Lys
	210					215					220				
Leu	Pro	Pro	Pro	Leu	Asn	Ile	Lys	Gly	Val	Arg	Ser	Phe	Leu	Gly	His
225					230					235				240	
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
			245						250						

<210> 140

<211> 762

<212> DNA

<213> Glycine max

<400> 140

gtgcgcaagg	aggttttgaa	gcttctagag	ggtgggctta	tctaccccat	ctccgacagc	60
gcttgggtaa	gcccagtcct	ggtggtgtcg	aagaaagagg	gcatgacagt	cattcgaaat	120
gaaaagaatg	acctgatacc	aacacgaact	gtcactagtt	ggaaattatg	catcgattac	180
cgcaagctca	acgaagccac	aaggaaagac	catttccctc	tacccttcat	ggatcagatg	240
ttggagagac	ttgcaggaca	cgcttattat	tgcttcttgg	atgcatactt	tggatataat	300
cagattgttg	tagaccccaa	ggatcaggag	aagatggcct	tcacatgccc	ttttggtgtc	360
tttgccctata	gacggattcc	at ttgggttg	tgcaatgcac	ctaccacatt	ccaaatgtgc	420
atgttggcca	tttttgcaga	tatagtggag	aaaagcatcg	aagtattcat	ggatgacttt	480
tcagtatttg	tgccctcatt	agaaagtgtg	ttgaagaagt	tggagatggg	actacaaaga	540
tgcgtggaaa	caaacttagt	actaaattgg	gagaagtgtc	acttcatggg	tcgagaaggc	600
atagtcttag	gccataaaat	ttcgacccca	ggaattgagg	tagaccaaac	aaagattgat	660
gtcattgaaa	agttgccacc	accatcaaat	gttaaaggca	tcaggagctt	cctaggacaa	720
gccaggttct	acagaagatt	catcaaggac	ttcacaaaag	tt		762

<210> 141

<211> 254

<212> PRT

<213> Glycine max

<400> 141

Val Arg Lys Glu Val Leu Lys Leu Leu Glu Val Gly Leu Ile Tyr Pro
 1 5 10 15
 Ile Ser Asp Ser Ala Trp Val Ser Pro Val Leu Val Val Ser Lys Lys
 20 25 30
 Glu Gly Met Thr Val Ile Arg Asn Glu Lys Asn Asp Leu Ile Pro Thr
 35 40 45
 Arg Thr Val Thr Ser Trp Lys Leu Cys Ile Asp Tyr Arg Lys Leu Asn
 50 55 60
 Glu Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Ala Gly His Ala Tyr Tyr Cys Phe Leu Asp Ala Tyr
 85 90 95
 Phe Gly Tyr Asn Gln Ile Val Val Asp Pro Lys Asp Gln Glu Lys Met
 100 105 110
 Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Ile Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Thr Thr Phe Gln Met Cys Met Leu Ala Ile
 130 135 140
 Phe Ala Asp Ile Val Glu Lys Ser Ile Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Phe Val Pro Ser Leu Glu Ser Cys Leu Lys Lys Leu Glu Met
 165 170 175
 Val Leu Gln Arg Cys Val Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Lys Ile Ser
 195 200 205
 Thr Arg Gly Ile Glu Val Asp Gln Thr Lys Ile Asp Val Ile Glu Lys
 210 215 220
 Leu Pro Pro Pro Ser Asn Val Lys Gly Ile Arg Ser Phe Leu Gly Gln
 225 230 235 240
 Ala Arg Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 142

<211> 762

<212> DNA

<213> Glycine max

<400> 142

gtgcggaagg aggttattaa gttgctagag gcagggctca tttacctaatt ctcagatagt 60
 tcatagggtta gtcctgttca tgggtgctctg aaaaaggagg gtatgacagt gataaagaat 120
 gatagagatg agttaattcc tacaagaata gttactggat ggaggatggg tattgattac 180
 aagaagctaa atgaagccac caggaaagac cattaccgc ttcccttcat ggatcaaagt 240
 cttgagagac ttgcagggca atcttcctac tatttattag atggatactc gggctacaat 300
 caaattgcag tggatcctca ggaccaagaa aagacagctt tcacatgtcc ttttggtgta 360
 tttgcttatc gccgcagtgc gttcgggttta tgtaatgccc caactacttt ccagagatgt 420
 atgatggcaa tttttgctga catggtaaag aaatgtattg aagtttttat ggacgatttc 480
 tctgtctttg gtgcattctt tgaaaattgc ctacgaaatt tagagaaagt gttacaacgc 540
 tatgaagaat ctaatttggg gctcaactgg gaaaaatgtc actttatggg tcaagaaggt 600
 atcatgctgg gacacaagat ttctagaaga ggaattaagg tggataaggc aaagattgag 660
 gttattgata aacttccacc tctagttaat gttagaggca tacgaagttt tttgggtcat 720
 gctagattct atcgatgatt tatcaaggac ttcaccaaag tt 762

<210> 143

<211> 254
 <212> PRT
 <213> Glycine max

<400> 143

Val	Arg	Lys	Glu	Val	Ile	Lys	Leu	Leu	Glu	Ala	Gly	Leu	Ile	Tyr	Leu
1				5					10					15	
Ile	Ser	Asp	Ser	Ser	Glx	Val	Ser	Pro	Val	His	Val	Ala	Leu	Lys	Lys
		20						25					30		
Gly	Gly	Met	Thr	Val	Ile	Lys	Asn	Asp	Arg	Asp	Glu	Leu	Ile	Pro	Thr
		35					40					45			
Arg	Ile	Val	Thr	Gly	Trp	Arg	Met	Gly	Ile	Asp	Tyr	Lys	Lys	Leu	Asn
	50					55				60					
Glu	Ala	Thr	Arg	Lys	Asp	His	Tyr	Pro	Leu	Pro	Phe	Met	Asp	Gln	Met
65					70				75					80	
Leu	Glu	Arg	Leu	Ala	Gly	Gln	Ser	Ser	Tyr	Tyr	Leu	Leu	Asp	Gly	Tyr
			85					90					95		
Ser	Gly	Tyr	Asn	Gln	Ile	Ala	Val	Asp	Pro	Gln	Asp	Gln	Glu	Lys	Thr
			100					105				110			
Ala	Phe	Thr	Cys	Pro	Phe	Gly	Val	Phe	Ala	Tyr	Arg	Arg	Met	Ser	Phe
	115					120					125				
Gly	Leu	Cys	Asn	Ala	Pro	Thr	Thr	Phe	Gln	Arg	Cys	Met	Met	Ala	Ile
	130					135					140				
Phe	Ala	Asp	Met	Val	Lys	Lys	Cys	Ile	Glu	Val	Phe	Met	Asp	Asp	Phe
145					150				155					160	
Ser	Val	Phe	Gly	Ala	Ser	Phe	Glu	Asn	Cys	Leu	Ala	Asn	Leu	Glu	Lys
			165					170					175		
Val	Leu	Gln	Arg	Tyr	Glu	Glu	Ser	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys
			180					185					190		
Cys	His	Phe	Met	Val	Gln	Glu	Gly	Ile	Met	Leu	Gly	His	Lys	Ile	Ser
	195						200				205				
Arg	Arg	Gly	Ile	Lys	Val	Asp	Lys	Ala	Lys	Ile	Glu	Val	Ile	Asp	Lys
	210					215					220				
Leu	Pro	Pro	Leu	Val	Asn	Val	Arg	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His
225					230				235					240	
Ala	Arg	Phe	Tyr	Arg	Glx	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
				245					250						

<210> 144
 <211> 761
 <212> DNA
 <213> Glycine max

<400> 144

gtgcggaagg	aggtccttaa	gttgctggaa	gcaggcctta	tttatcccat	ttcggatagt	60
gcatgggtta	gccctatgca	agttgtccct	aagaaaggag	gtatgacagt	cattaagaat	120
gataaagatg	agttgatatc	cacaaggacc	gtcaccgggt	ggagaatgtg	cattgactat	180
cgaaagctga	atgatgcacc	cggaaggacc	attatccact	ccctttcatg	ggccatatgc	240
ttgaaagact	tggtgggcaa	tcctattatt	gttttctaga	tgatattat	ggttataatc	300
agattgttgt	agatcccaaa	gatcaagaga	agacagcttt	cacctaccct	tttgggtgat	360
tcgcatatca	gtgcatgcct	tttgggtctat	gcaatgcccc	agctacattt	cagaggtgta	420
tgatggctat	tttttctgat	atgggtggaaa	tatgcattga	agttttcatg	gacgatttct	480
ctatttttgg	gccatccttt	gaagggtgct	tatcaaactt	tgaaaaagta	ttaaagagat	540
gtgaagagtc	caatctagtt	ctcaattgga	agaaatgcca	tttcatgggt	caagaaggaa	600
taatgttggg	gcataaaatt	tcagtaagag	ggatagaggt	ggacaaggca	aagattgatg	660
taattgagaa	actacttgct	cccatgaatg	tcaagggaat	aagaagcttc	ttaggacatg	720
cagggttcta	caggcgattc	ataaaagact	tcaccaaagt	t		761

<210> 145
 <211> 254
 <212> PRT
 <213> Glycine max

<400> 145
 Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro
 1 5 10 15
 Ile Ser Asp Ser Ala Trp Val Ser Pro Met Gln Val Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Val Ile Lys Asn Asp Lys Asp Glu Leu Ile Ser Thr
 35 40 45
 Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
 50 55 60
 Asp Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Gly His Met
 65 70 75 80
 Leu Glu Arg Leu Val Gly Gln Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Tyr Gly Tyr Asn Gln Ile Val Val Asp Pro Lys Asp Gln Glu Lys Thr
 100 105 110
 Ala Phe Thr Tyr Pro Phe Gly Val Phe Ala Tyr Gln Cys Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile
 130 135 140
 Phe Ser Asp Met Val Glu Ile Cys Ile Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Ile Phe Gly Pro Ser Phe Glu Gly Cys Leu Ser Asn Leu Glu Lys
 165 170 175
 Val Leu Lys Arg Cys Glu Glu Ser Asn Leu Val Leu Asn Trp Lys Lys
 180 185 190
 Cys His Phe Met Val Gln Glu Gly Ile Met Leu Gly His Lys Ile Ser
 195 200 205
 Val Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys
 210 215 220
 Leu Leu Ala Pro Met Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 146
 <211> 762
 <212> DNA
 <213> Glycine max

<400> 146
 gtgcgtaagg aggtgggtcaa gttgcttgaa gtaggactaa tttatccaat ctctgatagt 60
 gcttggggtga gttcgaacta ggtgggtgcct aagaaagggtg gtatgacggt gatccacaat 120
 gataagaatg atcttattcc tacacagaca atcattaggt ggcaaagtgt tattgactat 180
 cacaagttga atgatgtcac caagaaggac cattttcctc tgccattcat ggaccaaagt 240
 ttagagaggt tagctggcca agctttttat tgttttttgg atgggttattc tgggtataac 300
 caaatagcgg tgcattcttaa agatcaagag aagactacta tcatatgccc atttggtgtc 360
 tttgcttaca gacaaatgtc atttgaactg tgtaatgccc ctaccacctt ctagagattc 420
 atgatggcca tttttgctga ccttggtggag aaatgcatag aggtgttcat gaatgatttc 480
 tctatttttcg gctcttcctt ttatcattgt ttatccaacc tggaattagt gttacaacgg 540
 tgtgcggaaa ccaatttgtt gatgaactgg gagaaatgtc atttcatggt ccaagagggg 600
 attgtcttag gccacaagat ctcttcacaga ggggttgaag tggacaaggc aaaaattgat 660

gttattgaga agttgcctcc acctatgaat gtgaaaggca tccgaagttt tctcgaatat 720
 gttggatttt ataggaggtt catcaaagac ttcacgaaag tt 762

<210> 147
 <211> 254
 <212> PRT
 <213> Glycine max

<400> 147
 Val Arg Lys Glu Val Val Lys Leu Leu Glu Val Gly Leu Ile Tyr Pro
 1 5 10 15
 Ile Ser Asp Ser Ala Trp Val Ser Ser Asn Glx Val Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Val Ile His Asn Asp Lys Asn Asp Leu Ile Pro Thr
 35 40 45
 Gln Thr Ile Ile Arg Trp Gln Met Cys Ile Asp Tyr His Lys Leu Asn
 50 55 60
 Asp Val Thr Lys Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Ala Gly Gln Ala Phe Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Tyr Asn Gln Ile Ala Val His Leu Lys Asp Gln Glu Lys Thr
 100 105 110
 Thr Ile Ile Cys Pro Phe Gly Val Phe Ala Tyr Arg Gln Met Ser Phe
 115 120 125
 Glu Leu Cys Asn Ala Pro Thr Thr Phe Glx Arg Phe Met Met Ala Ile
 130 135 140
 Phe Ala Asp Leu Val Glu Lys Cys Ile Glu Val Phe Met Asn Asp Phe
 145 150 155 160
 Ser Ile Phe Gly Ser Ser Phe Tyr His Cys Leu Ser Asn Leu Glu Leu
 165 170 175
 Val Leu Gln Arg Cys Ala Glu Thr Asn Leu Leu Met Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser
 195 200 205
 Ser Arg Gly Leu Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys
 210 215 220
 Leu Pro Pro Pro Met Asn Val Lys Gly Ile Arg Ser Phe Leu Glu Tyr
 225 230 235 240
 Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 148
 <211> 762
 <212> DNA
 <213> Glycine max

<400> 148
 gtgcgtaagg aggttctcaa gcttttggag gttgggctca tatacctcat ctctgacagc 60
 gcttgggtaa gcctagtaca ggtggctccc aagaaatgcg gaatgacagt ggtacaaaat 120
 gagaggaatg acttgatacc aacacgaact gtcactggct agcggatgtg tatcgactac 180
 tgcaagttga atgaagccac acggaaggac catttcccct tacctttcat ggatcagatg 240
 ctggagaggc ttgcagggca ggcatactac tgtttcttgg atagatattc aggatacaac 300
 caaatcgcggt tagaccccag agatcaggag aagatggcct ttacatgccc ctttggcgtc 360
 tttgcttaca gaaggatgtc attcaggtta tgtaacgcac cagccacatt tcagagggtgc 420
 atgctggcca ttttttcaga catggtggag aagagcatcg aggtatttat ggatgaattc 480
 tcgatttttg gacccttatt tgacagttgc ttaaggaact tagagatggt actacagagg 540

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tcgcgtataga ctaacttgggt actaaattag gaaaaatgtc atttcatggt tgcgagagggg 600
atagtgatgg gccacaatat ctcagctaga gggattgagg ttgatcagac aaagatagac 660
gtcattgaga agttgccacc accactgaat gttaaaggcg tcagaagttt cttagggcat 720
gcaggtttct acaggagggt cataaaagac ttcacaaagg tt 762

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<210> 149
 <211> 254
 <212> PRT
 <213> Glycine max

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<400> 149
Val Arg Lys Glu Val Leu Lys Leu Leu Glu Val Gly Leu Ile Tyr Leu
 1           5           10           15
Ile Ser Asp Ser Ala Trp Val Ser Leu Val Gln Val Ala Pro Lys Lys
 20           25           30
Cys Gly Met Thr Val Val Gln Asn Glu Arg Asn Asp Leu Ile Pro Thr
 35           40           45
Arg Thr Val Thr Gly Glx Arg Met Cys Ile Asp Tyr Cys Lys Leu Asn
 50           55           60
Glu Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met
 65           70           75           80
Leu Glu Arg Leu Ala Gly Gln Ala Tyr Tyr Cys Phe Leu Asp Arg Tyr
 85           90           95
Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Arg Asp Gln Glu Lys Met
 100          105          110
Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Ser Phe
 115          120          125
Arg Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Leu Ala Ile
 130          135          140
Phe Ser Asp Met Val Glu Lys Ser Ile Glu Val Phe Met Asp Glu Phe
 145          150          155          160
Ser Ile Phe Gly Pro Leu Phe Asp Ser Cys Leu Arg Asn Leu Glu Met
 165          170          175
Val Leu Gln Arg Cys Val Glx Thr Asn Leu Val Leu Asn Glx Glu Lys
 180          185          190
Cys His Phe Met Val Arg Glu Gly Ile Val Met Gly His Asn Ile Ser
 195          200          205
Ala Arg Gly Ile Glu Val Asp Gln Thr Lys Ile Asp Val Ile Glu Lys
 210          215          220
Leu Pro Pro Pro Leu Asn Val Lys Gly Val Arg Ser Phe Leu Gly His
 225          230          235          240
Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245          250

```

<210> 150
 <211> 761
 <212> DNA
 <213> Glycine max

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<400> 150
gtgcgtaagg aggttttttaa gttgctggaa gcaggtctta tttatcccat ttcggatagt 60
gcatgggtta gccctgtgca ggttgtcccc aagaaagaag gtaagacagt cattaaggat 120
gaaaaggatg agttgatatc cacaaggact atcaccgggt ggagaatgtg cattgactat 180
cagaagctga atgatgccac ccggaaggac cattatccac tccctttcat ggaccaaag 240
cttgaaagac ttgccgggca atcttattat tgttttctgg atggatattc tggttataat 300
cagattgatg tagatcccaa ggatcaagag aagactgctt tcacctaccc ttttggtgta 360
ttcgccatc ggcgcagcc ctttggtttg tgcaatgccc cagctacatt tcagaggtgt 420

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atgatgacta ttttttctga tatggtggaa aaatgaattg aagttttcat ggacgatttc 480
tctatTTTTg ggccatcttt tgaagggtgc ttatcaaadc ttgaaagagt attaaagaga 540
cgtgaagagt ccaaactagt tctcaattgg gagaaatgcc atttcatggt tcaagaagga 600
atagtgtggg gcataaaaatt tcagtaagag ggatagaggt ggacaaggca aagattgatg 660
taatagagaa actacctcct cccatgaatg tcaagggaat aagaagcttc ctaggacatg 720
cagggttcta caagcgattc atcaaagatt tcacaaaggt t 761

```

<210> 151
 <211> 254
 <212> PRT
 <213> Glycine max

```

<400> 151
Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro
 1          5          10          15
Ile Ser Asp Ser Ala Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
          20          25          30
Glu Gly Lys Thr Val Ile Lys Asp Glu Lys Asp Glu Leu Ile Ser Thr
          35          40          45
Arg Thr Ile Thr Gly Trp Arg Met Cys Ile Asp Tyr Gln Lys Leu Asn
          50          55          60
Asp Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Asp Gln Met
          65          70          75          80
Leu Glu Arg Leu Ala Gly Gln Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr
          85          90          95
Ser Gly Tyr Asn Gln Ile Asp Val Asp Pro Lys Asp Gln Glu Lys Thr
          100          105          110
Ala Phe Thr Tyr Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Pro Phe
          115          120          125
Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Thr Ile
          130          135          140
Phe Ser Asp Met Val Glu Lys Glx Ile Glu Val Phe Met Asp Asp Phe
          145          150          155          160
Ser Ile Phe Gly Pro Ser Phe Glu Gly Cys Leu Ser Asn Leu Glu Arg
          165          170          175
Val Leu Lys Arg Arg Glu Glu Ser Lys Leu Val Leu Asn Trp Glu Lys
          180          185          190
Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser
          195          200          205
Val Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys
          210          215          220
Leu Pro Pro Pro Met Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
          225          230          235          240
Ala Gly Phe Tyr Lys Arg Phe Ile Lys Asp Phe Thr Lys Val
          245          250

```

<210> 152
 <211> 762
 <212> DNA
 <213> Glycine max

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<400> 152
gtgcggaaag aggtattcaa gttactagag gcagggtc tctacccaat ttcagatagc 60
tcctgggtta gtccggttca agttgttcca aaaaaaggag ggatgacagt ggtaaaaaat 120
gatagaaatg agctaattcc tacaagaaga gtcaccagat ggagaatgtg tattgattat 180
aggaagctca atgaagccac aagaaaagac cattacccac ttcccttcat ggatcaaag 240
cttaagagac ttgcaaggca atccttctac cgtttcttgg acggatactc aggttacaat 300

```

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cagattgcag tggatcctca ggatcaagaa aaaacagctt ttacatgtcc tttcagtgtt 360
tttgcttata gccgcatgcc gttcggttta tgtaatgcct ctactacttt tcagagatgt 420
atgatggcaa tttttgatga catggtagag aaatgtattg aagtctttat ggatgatttt 480
tcgttctttg gtgcattctt tggaaattgc ttagcaaatt tagagaaagt gttacaacgt 540
tgtgaaaaat ctaatttggt gcttaactgg gaaaaatgtc actttatggg acaagaaggt 600
attgtgctag gacacaaaat ctctaaaaga ggaattgagg tggttaaaga aaaactagat 660
gttattgata aacttcacc cccagttaat gtaaaaggca tacacagttt tttgggtcat 720
gttggatttt atcggcgatt cataaaggac ttcaccaaag tt 762

```

<210> 153
 <211> 254
 <212> PRT
 <213> Glycine max

```

<400> 153
Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro
 1          5          10          15
Ile Ser Asp Ser Ser Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
          20          25          30
Gly Gly Met Thr Val Val Lys Asn Asp Arg Asn Glu Leu Ile Pro Thr
          35          40          45
Arg Arg Val Thr Arg Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
          50          55          60
Glu Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Asp Gln Met
65          70          75          80
Leu Lys Arg Leu Ala Arg Gln Ser Phe Tyr Arg Phe Leu Asp Gly Tyr
          85          90          95
Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Gln Asp Gln Glu Lys Thr
          100          105          110
Ala Phe Thr Cys Pro Phe Ser Val Phe Ala Tyr Arg Arg Met Pro Phe
          115          120          125
Gly Leu Cys Asn Ala Ser Thr Thr Phe Gln Arg Cys Met Met Ala Ile
          130          135          140
Phe Asp Asp Met Val Glu Lys Cys Ile Glu Val Phe Met Asp Asp Phe
145          150          155          160
Ser Phe Phe Gly Ala Ser Phe Gly Asn Cys Leu Ala Asn Leu Glu Lys
          165          170          175
Val Leu Gln Arg Cys Glu Lys Ser Asn Leu Val Leu Asn Trp Glu Lys
          180          185          190
Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser
          195          200          205
Lys Arg Gly Ile Glu Val Val Lys Glu Lys Leu Asp Val Ile Asp Lys
          210          215          220
Leu Pro Pro Pro Val Asn Val Lys Gly Ile His Ser Phe Leu Gly His
225          230          235          240
Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
          245          250

```

<210> 154
 <211> 761
 <212> DNA
 <213> Glycine max

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<400> 154
gtgcgtaaag aagttttgaa gctgctagaa gcagacctta tttatcccat ttcggatagt 60
acatgggtta gccctgtgca agttgtcccc gagaaaggag gtatgacagt cattaagaat 120
gataaagatg agttgatatc cacaaggact gtcaccgggt gagaatgtgc attgactatc 180

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ggaagctgaa tgatgccacc cagaaggacc attattcact ccctttcatg gaccagatgc 240
ttgaaagact tgccggacaa tcctattatt gttttctgaa tggatactct ggctataatc 300
agatttggt agatcccaaa gatcaggaga aaactgcttt cacctgcctt tttggtgtat 360
ttgcatacaa gcgtatgcat tttggcttgt gtaatgctcc aactacgtgt cagaggtgta 420
tgatgactat tttttctggt atcgtggaaa aatgcattga acttttcatg gacgatttct 480
ctatttttgg gccatctttt gaaggctact tatcaaacct tgaaagagta ttacagagat 540
gtgaagagtc taatctagtt ctcaattggg agaaatgcca tttcatgggt caagaaggaa 600
tagtgctggg gcataaaatt tcagtaagag ggatagaggt ggacaaggca aagattgatg 660
taattgagaa actacctcct cccatgattg tcaagggaat aagaagcctc ctaggacatg 720
tagggttcta caggcgattc atcaaagact tcacaaagggt t 761

```

<210> 155

<211> 254

<212> PRT

<213> Glycine max

<400> 155

```

Val Arg Lys Glu Val Leu Lys Leu Leu Glu Ala Asp Leu Ile Tyr Pro
 1           5           10           15
Ile Ser Asp Ser Thr Trp Val Ser Pro Val Gln Val Val Pro Glu Lys
          20           25           30
Gly Gly Met Thr Val Ile Lys Asn Asp Lys Asp Glu Leu Ile Ser Thr
          35           40           45
Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
          50           55           60
Asp Ala Thr Gln Lys Asp His Tyr Ser Leu Pro Phe Met Asp Gln Met
65           70           75           80
Leu Glu Arg Leu Ala Gly Gln Ser Tyr Tyr Cys Phe Leu Asn Gly Tyr
          85           90           95
Ser Gly Tyr Asn Gln Ile Val Val Asp Pro Lys Asp Gln Glu Lys Thr
          100          105          110
Ala Phe Thr Cys Leu Phe Gly Val Phe Ala Tyr Lys Arg Met His Phe
          115          120          125
Gly Leu Cys Asn Ala Pro Thr Thr Cys Gln Arg Cys Met Met Thr Ile
          130          135          140
Phe Ser Gly Ile Val Glu Lys Cys Ile Glu Leu Phe Met Asp Asp Phe
145          150          155          160
Ser Ile Phe Gly Pro Ser Phe Glu Gly Tyr Leu Ser Asn Leu Glu Arg
          165          170          175
Val Leu Gln Arg Cys Glu Glu Ser Asn Leu Val Leu Asn Trp Glu Lys
          180          185          190
Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser
          195          200          205
Val Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys
210          215          220
Leu Pro Pro Pro Met Ile Val Lys Gly Ile Arg Ser Leu Leu Gly His
225          230          235          240
Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
          245          250

```

<210> 156

<211> 762

<212> DNA

<213> Glycine max

<400> 156

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gtgctgaagg aggttttttaa gttgctggaa gcaggtctta tttatcccat ttcggatagt

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60

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gcatgggtta gccctgtgca ggttggtcccc aagaaagaag gtaagacagt cattaaggat 120
gaaaaagatg agttgatatc cacaaggact atcacggggt ggagaatgtg cattgactat 180
cagaagctga atgatgccac ccggaaggac cattatccac tccctttcat ggaccaaagt 240
cttgaaagac ttgccgggca atcttattat tgttttcttg atggatattc tgggtataat 300
cagattgatg tagatcccaa ggatcaagag aagactgctt tcacctacc ttttggtgta 360
ttcgctatc ggccatgccc ctttggtttg tgcaatgccc cagctacatt tcagaggtgt 420
atgatgacta ttttttctga tatgggtggaa aaatgaattg aagttttcat ggacgatgtc 480
tctatttttg ggccatcttt tgaagggtgc ttatcaaadc ttgaaagagt attaaagaga 540
cgtgaagagt ccaaactagt tctcaattgg gagaaatgcc atttcatggt tcaagaagga 600
atagtgttgg ggcatataaat ttcagtaaga gggatagagg tggacaaggc aaagattgat 660
gtaatagaga aactacctcc tcccatgaat gtcaagggaa taagaagctt cctaggacat 720
gcaggggttct acaagcgatt catcaaagac ttctcaaaag tt 762

```

<210> 157
 <211> 254
 <212> PRT
 <213> Glycine max

```

<400> 157
Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro
1      5      10      15
Ile Ser Asp Ser Ala Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
20     25     30
Glu Gly Lys Thr Val Ile Lys Asp Glu Lys Asp Glu Leu Ile Ser Thr
35     40     45
Arg Thr Ile Thr Gly Trp Arg Met Cys Ile Asp Tyr Gln Lys Leu Asn
50     55     60
Asp Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Asp Gln Met
65     70     75     80
Leu Glu Arg Leu Ala Gly Gln Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr
85     90     95
Ser Gly Tyr Asn Gln Ile Asp Val Asp Pro Lys Asp Gln Glu Lys Thr
100    105    110
Ala Phe Thr Tyr Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Pro Phe
115    120    125
Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Thr Ile
130    135    140
Phe Ser Asp Met Val Glu Lys Glx Ile Glu Val Phe Met Asp Asp Val
145    150    155    160
Ser Ile Phe Gly Pro Ser Phe Glu Gly Cys Leu Ser Asn Leu Glu Arg
165    170    175
Val Leu Lys Arg Arg Glu Glu Ser Lys Leu Val Leu Asn Trp Glu Lys
180    185    190
Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser
195    200    205
Val Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys
210    215    220
Leu Pro Pro Pro Met Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
225    230    235    240
Ala Gly Phe Tyr Lys Arg Phe Ile Lys Asp Phe Ser Lys Val
245    250

```

<210> 158
 <211> 761
 <212> DNA
 <213> Glycine max

<400> 158

```

gtgcggaagg aggttcttaa gtccttgga gagggtctca tctatcttat ctcagatagt      60
gttgggtgag tccagtgcac gtggttccca agaaggggtg gaagactgtg gtgagaaatg      120
agaaaaatga cctcattcta acccgaactg tcacaggatg gagaatgtgc atagattatc      180
ggaagttgaa tgatgccatc aagaaggatc acttccctct accattcata gatcagatgc      240
ttgagagggt agcaagccag tctttctatt atttcttgga tgaatattct agatacaatc      300
agattgctat acatcccaag gaccaagaga agattgcatt tacatgcca tttggtgtct      360
ttgcctatag aaggatgcca ttgaactat gcaatgctcc agctaccttt tagaggcata      420
tgctagccat attcgctaac atgggtggaga aatgcatcga agtggtcata gatgattttt      480
cgggtgttgg tccatccttt gtttgttgtt tgaccaatttt agagctagtg ttgaagtact      540
gtgaggagac aaatttagta ttgaattggg agaaatgtca tttcatgggt caagaaggaa      600
ttatgttggg gcataaaatt tttgctagag gtattgaggt ggacaaggcc aaaattgatg      660
ttattgaaaa gctgcctcca ccagtcaatg taaaaggcat caggagtttt cttggacaca      720
ctggtttctt caggcgtttc atcaaggact tcacaaaagt t                                761

```

<210> 159

<211> 254

<212> PRT

<213> Glycine max

<400> 159

```

Val Arg Lys Glu Val Leu Lys Leu Leu Glu Ala Gly Leu Ile Tyr Leu
 1          5          10          15
Ile Ser Asp Ser Ala Trp Val Ser Pro Val His Val Val Pro Lys Lys
 20          25          30
Gly Gly Lys Thr Val Val Arg Asn Glu Lys Asn Asp Leu Ile Leu Thr
 35          40          45
Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
 50          55          60
Asp Ala Ile Lys Lys Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met
 65          70          75          80
Leu Glu Arg Leu Ala Ser Gln Ser Phe Tyr Tyr Phe Leu Asp Glu Tyr
 85          90          95
Ser Arg Tyr Asn Gln Ile Ala Ile His Pro Lys Asp Gln Glu Lys Ile
100          105          110
Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Pro Phe
115          120          125
Glu Leu Cys Asn Ala Pro Ala Thr Phe Glx Arg His Met Leu Ala Ile
130          135          140
Phe Ala Asn Met Val Glu Lys Cys Ile Glu Val Phe Ile Asp Asp Phe
145          150          155          160
Ser Val Phe Gly Pro Ser Phe Val Cys Cys Leu Thr Asn Leu Glu Leu
165          170          175
Val Leu Lys Tyr Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
180          185          190
Cys His Phe Met Val Gln Glu Gly Ile Met Leu Gly His Lys Ile Phe
195          200          205
Ala Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys
210          215          220
Leu Pro Pro Pro Val Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
225          230          235          240
Thr Gly Phe Phe Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
245          250

```

<210> 160

<211> 762

<212> DNA

<213> Pisum sativum

<400> 160

```

gtgcgcaagg aagtactcaa gttgttagat tcgggaatga tttaccccat ttctgacagc      60
tcgtgggtaa gtccagtga cgtggtacca aagaaaggag gaacctcagt aattttaaat      120
gaaaagaatg aactgatccc aactcgaca gtgacagggt ggcgagtatg catcgatcac      180
agaagactga acacagcaac aagaaaggat cattttcctc tcccttttat tgatcaaatg      240
ttagaaagac ttgcagggtca tgagtattat tgctttctgg atggatattc gggatacaat      300
caaattgttg tagccccgga agatcaggaa aaaactgcat ttacatgtcc ttatggtatt      360
ttcgcttaca gacggatgcc atttgggcta tgcaatgccc cagctacttt tcagagggtg      420
atgacatcta tattctccga catgcttgaa aagtatatga aggtgtttat ggatgatttc      480
tctgtgtttg gttcttcttt tgataattgt ttagctaact tgtctcttgt tttgcaaaga      540
tgtcaggaaa ctaaccttgt tctcaattgg gagaaatgtc atttcatggg gcaggaagga      600
attgtgctag gacacaaaat ttcccacaaa ggaattgaag tggacaaagc caaagtggag      660
gttatagcta acctcccacc tccggtgaat gaaaaaggga taaggagttt tttgggtcat      720
gcaggttttt atcgcagggt catcaaagac ttcacaaagg tt                          762

```

<210> 161

<211> 254

<212> PRT

<213> Pisum sativum

<400> 161

```

Val Arg Lys Glu Val Leu Lys Leu Leu Asp Ser Gly Met Ile Tyr Pro
1          5          10          15
Ile Ser Asp Ser Trp Val Ser Pro Val His Val Val Pro Lys Lys
20          25          30
Gly Gly Thr Ser Val Ile Leu Asn Glu Lys Asn Glu Leu Ile Pro Thr
35          40          45
Arg Thr Val Thr Gly Trp Arg Val Cys Ile Asp His Arg Arg Leu Asn
50          55          60
Thr Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met
65          70          75          80
Leu Glu Arg Leu Ala Gly His Glu Tyr Tyr Cys Phe Leu Asp Gly Tyr
85          90          95
Ser Gly Tyr Asn Gln Ile Val Val Ala Pro Glu Asp Gln Glu Lys Thr
100          105          110
Ala Phe Thr Cys Pro Tyr Gly Ile Phe Ala Tyr Arg Arg Met Pro Phe
115          120          125
Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Thr Ser Ile
130          135          140
Phe Ser Asp Met Leu Glu Lys Tyr Met Lys Val Phe Met Asp Asp Phe
145          150          155          160
Ser Val Phe Gly Ser Ser Phe Asp Asn Cys Leu Ala Asn Leu Ser Leu
165          170          175
Val Leu Gln Arg Cys Gln Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
180          185          190
Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser
195          200          205
His Lys Gly Ile Glu Val Asp Lys Ala Lys Val Glu Val Ile Ala Asn
210          215          220
Leu Pro Pro Pro Val Asn Glu Lys Gly Ile Arg Ser Phe Leu Gly His
225          230          235          240
Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
245          250

```

<210> 162

<211> 762
 <212> DNA
 <213> Pisum sativum

<400> 162
 gtgcgtaagg aggtctttaa actattggat gcgggaatga tttacccgat ctcggatagt 60
 ccgtgggtta gtcccgtgca cgtgggtccg aagaaggggtg gaatgaccgt aatccgtaat 120
 gacaaagacg aattgatccc gactaaagtt gcaacggggt ggagaatatg tatagattat 180
 agacagttga ataccgcgac tcgaaaggac cattttccac tcccatttat ggatcaaagt 240
 cttgaaagac tatcggggcca acaatactat tgtttcttgg acggctactc cgggtacaac 300
 caaattgcgg ttgacccggt tgatcatgag aagacggctt tcacgtgtcc gtttggagtg 360
 ttcgcataca gaaaaatgcc ctttgggctg tgcaatgcac cggcgacttt ccaacgatgc 420
 gtcctagcca tttttgccga tctaataagag aaaacaatgg acgtcttcat ggatgacttc 480
 tcggtatttg gtgggacgtt tagtctatgc ttggcaaatt tgaagacggg gttggaaagg 540
 tgtgtgaaga ccaatttggg gctaaattgg gaaaagtgtc acttcatggg gaccgagggg 600
 atcgtgctag gccacaaagt ctctaaaagg gggcttgaag tggatagagc taaggttgaa 660
 gtaattgaaa aattaccccc tccggtgaat gtgaaaggca tccgtagctt tttggggcac 720
 gcgggggtttt accggcgctt cattaaagac ttctcaaaag tt 762

<210> 163
 <211> 254
 <212> PRT
 <213> Pisum sativum

<400> 163
 Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Met Ile Tyr Pro
 1 5 10 15
 Ile Ser Asp Ser Pro Trp Val Ser Pro Val His Val Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Val Ile Arg Asn Asp Lys Asp Glu Leu Ile Pro Thr
 35 40 45
 Lys Val Ala Thr Gly Trp Arg Ile Cys Ile Asp Tyr Arg Gln Leu Asn
 50 55 60
 Thr Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Ser Gly Gln Gln Tyr Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Val Asp His Glu Lys Thr
 100 105 110
 Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Lys Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Val Leu Ala Ile
 130 135 140
 Phe Ala Asp Leu Ile Glu Lys Thr Met Asp Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Phe Gly Gly Thr Phe Ser Leu Cys Leu Ala Asn Leu Lys Thr
 165 170 175
 Val Leu Glu Arg Cys Val Lys Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Thr Glu Gly Ile Val Leu Gly His Lys Val Ser
 195 200 205
 Lys Arg Gly Leu Glu Val Asp Arg Ala Lys Val Glu Val Ile Glu Lys
 210 215 220
 Leu Pro Pro Pro Val Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Ser Lys Val
 245 250

<210> 164
 <211> 762
 <212> DNA
 <213> Pisum sativum

<400> 164
 gtgcggaagg aggtctttaa attggttgat gcgggggatga tttacccgat ctcggatagt 60
 ccatgggtta gtctgtgca cgttgttccg aagaagggggg ggattaccgt aatccggaat 120
 gacaaggatg aattgatccc cactaaagtt gaaacggggg ggagaatgtg tattgattat 180
 aggcgggttg ataccgcgac tcgaaaagac cattttccac tcccatttat ggatcaaagt 240
 ctcgaaagac tatcgggcca acaatattat tgttttttgg acggctactc cgggtacaac 300
 caaattgcgg ttgacccggc cgatcatgag aagacggctt tcacatgtcc gtttggagtg 360
 ttcgcatacc gaaaaatgcc ctttgggctg tgcaatgcac cggcgacctt ccaacgatgt 420
 gtccaagcca tttttgtcga tctgatagag aaaacaatgg aagtcttcat ggatgacttc 480
 tcggtatttg gtgggtcttt tagtctatgc ttggcgaact tgaaaacggg gttggagaga 540
 tgtgtgaaga ccaatttggg gcttaattgg gagaagtgtc acttcatggg gaccgagggg 600
 atcgtgctag gccacaaagt ctctagaagg gggcttgaag tggatagagc taaggttgaa 660
 gtgatagaaa aattacctcc tccgggtgaat gtgaagggca tccgaagctt tttggggcac 720
 gccgggttct accggcgctt cattaagat ttcacaaagg tt 762

<210> 165
 <211> 254
 <212> PRT
 <213> Pisum sativum

<400> 165
 Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Met Ile Tyr Pro
 1 5 10 15
 Ile Ser Asp Ser Pro Trp Val Ser Pro Val His Val Val Pro Lys Lys
 20 25 30
 Gly Gly Ile Thr Val Ile Arg Asn Asp Lys Asp Glu Leu Ile Pro Thr
 35 40 45
 Lys Val Glu Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Arg Leu Asn
 50 55 60
 Thr Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Ser Gly Gln Gln Tyr Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Ala Asp His Glu Lys Thr
 100 105 110
 Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Lys Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Val Gln Ala Ile
 130 135 140
 Phe Val Asp Leu Ile Glu Lys Thr Met Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Phe Gly Gly Ser Phe Ser Leu Cys Leu Ala Asn Leu Lys Thr
 165 170 175
 Val Leu Glu Arg Cys Val Lys Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Thr Glu Gly Ile Val Leu Gly His Lys Val Ser
 195 200 205
 Arg Arg Gly Leu Glu Val Asp Arg Ala Lys Val Glu Val Ile Glu Lys
 210 215 220
 Leu Pro Pro Pro Val Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 166
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated oligonucleotide

<221> misc_feature
 <222> 6, 15, 16, 18
 <223> n = A,T,C or G

<400> 166
 gtgcgnaarg argtnntnaa ryt

23

<210> 167
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> plant retroelement sequence

<400> 167
 Val Arg Lys Glu Val Leu Lys Leu
 1 5

<210> 168
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated oligonucleotide

<221> misc_feature
 <222> 7
 <223> n = A,T,C or G

<400> 168
 aacyttngwr aartcyttta traa

24

<210> 169
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> plant retroelement sequence

<400> 169
 Val Lys Ser Phe Asp Lys Ile Phe
 1 5

<210> 170
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 170
 gggatccgca attagaatct

20

<210> 171
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 171
 cgaattcggc ccacttcgga

20

<210> 172
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 172
 ccacaagatt ctaattgcgg attc

24

<210> 173
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 173
 ccgaaatgga ccgaacccga catc

24

<210> 174
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 174
 tttccaggct cttgacgaga tttg

24

<210> 175
 <211> 22

<212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 175
 cgactcgagc tccatagcga tg 22

<210> 176
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 176
 cggattgggc cgaaatggac cgaa 24

<210> 177
 <211> 18
 <212> DNA
 <213> Arabidopsis thaliana

<400> 177
 gaggacttgg ggggcaaa 18

<210> 178
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> exemplary motif

<221> VARIANT
 <222> 2-3, 5-7, 9-12
 <223> Xaa = Any Amino Acid

<400> 178
 Cys Xaa Xaa Cys Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Cys
 1 5 10

<210> 179
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> exemplary motif

<400> 179
 Leu Ile Asp Leu Gly Ala
 1 5

<210> 180

<211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<400> 180
 Lys Thr Ala Phe
 1

<210> 181
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<221> VARIANT
 <222> 2
 <223> Xaa = Pro or Ser

<400> 181
 Met Xaa Phe Gly Leu Cys Asn Ala
 1 5

<210> 182
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<221> VARIANT
 <222> 1
 <223> Xaa = Val, Ile, or Met

<221> VARIANT
 <222> 9
 <223> Xaa = Ser or Trp

<221> VARIANT
 <222> 10
 <223> Xaa = Val or Ile

<400> 182
 Xaa·Glu Val Phe Met Asp Asp Phe Xaa Xaa
 1 5 10

<210> 183
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>

<223> consensus sequence

<221> VARIANT

<222> 12

<223> Xaa = Ile or Val

<400> 183

Phe Glu Leu Met Cys Asp Ala Ser Asp Tyr Ala Xaa Gly Ala Val Leu
 1 5 10 15
 Gly Gln Arg

<210> 184

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<221> VARIANT

<222> 4

<223> Xaa = Thr or Ile

<221> VARIANT

<222> 8

<223> Xaa = Leu or Met

<221> VARIANT

<222> 13

<223> Xaa = Phe or Tyr

<221> VARIANT

<222> 15

<223> Xaa = Leu or Phe

<221> VARIANT

<222> 19

<223> Xaa = Arg or Lys

<221> VARIANT

<222> 23

<223> Xaa = Ile or Val

<221> VARIANT

<222> 26

<223> Xaa = Arg or Lys

<400> 184

Tyr Ala Thr Xaa Glu Lys Glu Xaa Leu Ala Ile Val Xaa Ala Xaa Glu
 1 5 10 15
 Lys Phe Xaa Ser Tyr Leu Xaa Gly Ser Xaa Val
 20 25

<210> 185

<211> 46

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<221> VARIANT

<222> 4, 6-7, 11-40, 43

<223> Xaa = Any Amino Acid

<400> 185

His	Cys	His	Xaa	Ser	Xaa	Xaa	Gly	Gly	His	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5					10					15		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25					30			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Asp	Xaa	Cys	Gln	Arg			
			35				40					45				

<210> 186

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<221> VARIANT

<222> 6

<223> Xaa = Ile, Val, or Met

<400> 186

Trp	Gly	Ile	Asp	Phe	Xaa	Gly	Pro
1				5			

<210> 187

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<221> VARIANT

<222> 7

<223> Xaa = Any Amino Acid

<221> VARIANT

<222> 10

<223> Xaa = Ala or Val

<400> 187

Pro	Tyr	His	Pro	Gln	Thr	Xaa	Gly	Gln	Xaa	Glu
1				5				10		

<210> 188

<211> 13

<212> DNA

<213> Artificial Sequence

<220>
 <223> consensus sequence

<221> misc_feature
 <222> 11, 12
 <223> n = A,T,C or G

<400> 188
 atttgggggra nnt

13

<210> 189
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<221> VARIANT
 <222> 5, 8
 <223> Xaa = Arg or Lys

<400> 189
 Gln Met Ala Ser Xaa Lys Arg Xaa Ala
 1 5

<210> 190
 <211> 6
 <212> PRT
 <213> Pisum sativum

<400> 190
 Ala Ser Lys Lys Arg Lys
 1 5